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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:38:42 ; Search time 166 Seconds
(without alignments)
2458.836 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPRAPRCRAVRSLLRSHYRE.....TALEAANPALPSDFKTLTD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	9	US-09-990-080-2
2	5961	100.0	1132	9	US-09-749-728B-31
3	5961	100.0	1132	9	US-09-843-676-225
4	5961	100.0	1132	9	US-09-953-052-2
5	5961	100.0	1132	11	US-09-788-110A-23
6	5961	100.0	1132	14	US-10-053-758-225
7	5961	100.0	1132	14	US-10-208-243-2
8	5961	100.0	1132	14	US-10-054-295-225
9	5961	100.0	1132	14	US-10-054-611-225
10	5961	100.0	1132	14	US-10-105-961-2
11	5961	100.0	1132	14	US-10-044-692-2
12	5961	100.0	1132	14	US-10-044-539-2
13	5961	100.0	1132	14	US-10-295-681-57

14	5961	100.0	1132	14	US-10-325-810-2	Sequence 2, Appli
15	5961	100.0	1132	14	US-10-388-578-2	Sequence 2, Appli
16	5961	100.0	1132	16	US-10-602-441-2	Sequence 2, Appli
17	5961	100.0	1132	16	US-10-389-431-2	Sequence 2, Appli
18	5961	100.0	1132	17	US-10-877-124-2	Sequence 2, Appli
19	5961	100.0	1132	17	US-10-877-022-2	Sequence 2, Appli
20	5961	100.0	1132	17	US-10-862-698-3	Sequence 3, Appli
21	5961	100.0	1154	14	US-10-044-539-323	Sequence 323, App
22	5961	100.0	1154	14	US-10-044-539-323	Sequence 323, App
23	5961	100.0	1154	14	US-10-325-810-611	Sequence 611, App
24	5961	100.0	1154	17	US-10-877-124-611	Sequence 611, App
25	5961	100.0	1154	17	US-10-877-022-611	Sequence 611, App
26	5961	100.0	1189	14	US-10-044-692-325	Sequence 325, App
27	5961	100.0	1189	14	US-10-044-539-325	Sequence 325, App
28	5961	100.0	1189	14	US-10-325-810-613	Sequence 613, App
29	5961	100.0	1189	17	US-10-877-124-613	Sequence 613, App
30	5961	100.0	1189	17	US-10-877-022-613	Sequence 613, App
31	5961	100.0	1200	14	US-10-044-692-324	Sequence 324, App
32	5961	100.0	1200	14	US-10-044-539-324	Sequence 324, App
33	5961	100.0	1200	14	US-10-325-810-612	Sequence 612, App
34	5961	100.0	1200	17	US-10-877-124-612	Sequence 612, App
35	5961	100.0	1200	17	US-10-877-022-612	Sequence 612, App
36	5961	100.0	1285	14	US-10-044-692-314	Sequence 314, App
37	5961	100.0	1285	14	US-10-044-539-314	Sequence 314, App
38	5961	100.0	1285	14	US-10-325-810-600	Sequence 600, App
39	5961	100.0	1285	17	US-10-877-124-600	Sequence 600, App
40	5961	100.0	1285	17	US-10-877-022-600	Sequence 600, App
41	5954	99.9	1132	14	US-10-385-882-2	Sequence 2, Appli
42	5952	99.8	1132	14	US-10-325-810-344	Sequence 344, App
43	5952	99.8	1132	17	US-10-877-124-344	Sequence 344, App
44	5952	99.8	1132	17	US-10-877-022-344	Sequence 344, App
45	5952	99.8	1407	14	US-10-044-692-334	Sequence 334, App

ALIGNMENTS

RESULT 1

US-09-990-080-2
; Sequence 2, Application US/09990080
; Patent No. US2002010286A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-080-2

Query Match	100.0%	Score	5961	DB	9	Length	1132
Best Local Similarity	100.0%	Pred. No.	0				
Matches	1132	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGWRLVORGDPAAFRALVAQCLVCVPW	60				
Db	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGWRLVORGDPAAFRALVAQCLVCVPW	60				
Qy	61	DARPPAAPFRQVSCIKELVARVLQRLCERGAKNVLAFLGFDGARGSPPEAFTTSVR	120				
Db	61	DARPPAAPFRQVSCIKELVARVLQRLCERGAKNVLAFLGFDGARGSPPEAFTTSVR	120				
Qy	121	SYLNTVTDLRGSGANGLLLRVGGDVLVHLLARCAFLVLVAPSCAYQVCGPPLYQLGA	180				
Db	121	SYLNTVTDLRGSGANGLLLRVGGDVLVHLLARCAFLVLVAPSCAYQVCGPPLYQLGA	180				

QY	181	ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLP	AGARRGG	SASRSLPLPKPRR	240	
DB	181	ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLP	AGARRGG	SASRSLPLPKPRR	240	
QY	241	GAAPPERTPVQGSWAHPGRTRGSDRGFCVSPARPAE	EATSL	EGALSGTRHSHPSVG	300	
DB	241	GAAPPERTPVQGSWAHPGRTRGSDRGFCVSPARPAE	EATSL	EGALSGTRHSHPSVG	300	
QY	301	RQHAGPSTSRPPRPWDTPCOPVYAEKHF	LYSSGDK	EQLRPSFLSSLRPSLTGARRL	360	
DB	301	RQHAGPSTSRPPRPWDTPCOPVYAEKHF	LYSSGDK	EQLRPSFLSSLRPSLTGARRL	360	
QY	361	VETIFLGRPMWPGTFRRLPRLPQRYWQMRPLF	LELLGNHQAQCPYGV	LLKTHCPRAAAVT	420	
DB	361	VETIFLGRPMWPGTFRRLPRLPQRYWQMRPLF	LELLGNHQAQCPYGV	LLKTHCPRAAAVT	420	
QY	421	PAAGVCAREKPGQGSVAAPEEEDTDPRRLVQLLR	QHSSPWQYVGFVRA	CLRLRVPGLWGS	480	
DB	421	PAAGVCAREKPGQGSVAAPEEEDTDPRRLVQLLR	QHSSPWQYVGFVRA	CLRLRVPGLWGS	480	
QY	481	RHNERRFLRNTKFTISLGKHA	KLSELTWKMSVRDCAWLR	RRSPGVCVPAAEHLRREI	540	
DB	481	RHNERRFLRNTKFTISLGKHA	KLSELTWKMSVRDCAWLR	RRSPGVCVPAAEHLRREI	540	
QY	541	LAKFLHLMMSYVYVELLRSFFYVTETTFQKNR	LFFYRKSVMKLSQSIGI	GRHQLKRVOLRE	600	
DB	541	LAKFLHLMMSYVYVELLRSFFYVTETTFQKNR	LFFYRKSVMKLSQSIGI	GRHQLKRVOLRE	600	
QY	601	LSEAEVRQHREAR	PALLTSRLRFTPKPDGLRPI	VNMDYVVGARTFRREKRAERLTSRVKA	660	
DB	601	LSEAEVRQHREAR	PALLTSRLRFTPKPDGLRPI	VNMDYVVGARTFRREKRAERLTSRVKA	660	
QY	661	LFSVLNTERARRPGLLGASVLGLDDI	IHRWRTFVL	RAODPPPELYFVKVDVTGAYDTI	720	
DB	661	LFSVLNTERARRPGLLGASVLGLDDI	IHRWRTFVL	RAODPPPELYFVKVDVTGAYDTI	720	
QY	721	PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL			780	
DB	721	PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL			780	
QY	781	QETSPLRDVA	IVIEOSSSINEASSGLFDVFLR	FMCHHAVIRGKSYVOCQIGIPGGSILSTL	840	
DB	781	QETSPLRDVA	IVIEOSSSINEASSGLFDVFLR	FMCHHAVIRGKSYVOCQIGIPGGSILSTL	840	
QY	841	LCSLCYGD	MENKLFAGIRRDGLLLRLVDDFL	LVTPHLTHAKTFLRTLVRGVP	EGCVNVL	900
DB	841	LCSLCYGD	MENKLFAGIRRDGLLLRLVDDFL	LVTPHLTHAKTFLRTLVRGVP	EGCVNVL	900
QY	901	RKTVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLE	VQSDYSSYARTSIRASLTF		960	
DB	901	RKTVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLE	VQSDYSSYARTSIRASLTF		960	
QY	961	NRGFKAGNRMRKLFVGLRLKCHSLFDLDQVNS	LQVCTNIIKILLQAYRHACVLQLP		1020	
DB	961	NRGFKAGNRMRKLFVGLRLKCHSLFDLDQVNS	LQVCTNIIKILLQAYRHACVLQLP		1020	
QY	1021	FHQQVWKNPTFFLRLV	ISDTASLCYSILKAKNAGMSLGAKG	AGPLPSEAVQWLCHQAFLL	1080	
DB	1021	FHQQVWKNPTFFLRLV	ISDTASLCYSILKAKNAGMSLGAKG	AGPLPSEAVQWLCHQAFLL	1080	
QY	1081	KLTRHRVYVPLLGSLRTAQQLSRKLP	GGTTLTAL	EAAAANPALPSDFKTILD	1132	
DB	1081	KLTRHRVYVPLLGSLRTAQQLSRKLP	GGTTLTAL	EAAAANPALPSDFKTILD	1132	

RESULT 2

US-09-749-728B-31
; Sequence 31, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-ichi

; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOM
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749, 728B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-011148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 31
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-749-728B-31

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1132;		Conservative		0;		Mismatches		0;		Indels		0;		Gaps		0;													
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DB	1	MPRAPRCRAVR	SLLRSHYREV	LP	ATFVRR	LG	PQGWRLV	Q	R	G	D	P	A	A	F	R	A	L	V	A	Q	C	L	V	C	V	P	W	60
QY	61	DARPPAAP	SFQVSLCKEL	VARVLQ	RLCERGA	KNVLA	FGFALL	LDGARG	GGPPEA	FTTSVR	120																		
DB	61	DARPPAAP	SFQVSLCKEL	VARVLQ	RLCERGA	KNVLA	FGFALL	LDGARG	GGPPEA	FTTSVR	120																		
QY	121	SYLPTNTV	TDALRG	SGAWGL	LLRRVGD	VDVLLH	LARCAL	FVLVAP	SCAYQ	VCGGPPL	YQLGA	180																	
DB	121	SYLPTNTV	TDALRG	SGAWGL	LLRRVGD	VDVLLH	LARCAL	FVLVAP	SCAYQ	VCGGPPL	YQLGA	180																	
QY	181	ATQARPP	PHASGPR	RLRG	CERAWN	HSVREAG	VPGLG	PA	GARRRG	GSASRS	LPLPKPRR	240																	
DB	181	ATQARPP	PHASGPR	RLRG	CERAWN	HSVREAG	VPGLG	PA	GARRRG	GSASRS	LPLPKPRR	240																	
QY	241	GAAPPERT	TPVQGS	WAHPGR	TRGSDRG	FCVSPAR	PAEATSL	EGALSG	TRHSHPS	VG	300																		
DB	241	GAAPPERT	TPVQGS	WAHPGR	TRGSDRG	FCVSPAR	PAEATSL	EGALSG	TRHSHPS	VG	300																		
QY	301	RQHAGP	STSRPP	RPWDTP	PCPPVYAE	TKHF	LYSSGDK	EQLRPS	FLLSLRPS	LTGARRL	360																		
DB	301	RQHAGP	STSRPP	RPWDTP	PCPPVYAE	TKHF	LYSSGDK	EQLRPS	FLLSLRPS	LTGARRL	360																		
QY	361	VETIFLGR	PMWPGTFR	RLPLRPL	PQRYWQMR	PLFLELLGNHQAQCPYGV	LLKTHCP	RAAVT	420																				
DB	361	VETIFLGR	PMWPGTFR	RLPLRPL	PQRYWQMR	PLFLELLGNHQAQCPYGV	LLKTHCP	RAAVT	420																				
QY	421	PAAGVCAREKPGQGS	VAAPEEEDTDPRRLVQLLR	QHSFPWQYVGFVRA	CLRLRVP	GLWGS	480																						
DB	421	PAAGVCAREKPGQGS	VAAPEEEDTDPRRLVQLLR	QHSFPWQYVGFVRA	CLRLRVP	GLWGS	480																						
QY	481	RHNERRFURN	TKKFTSLGKHAKLSLOELTW	KMSVRDCAWLR	RRSPGVCV	PAAEHLRREI	540																						
DB	481	RHNERRFURN	TKKFTSLGKHAKLSLOELTW	KMSVRDCAWLR	RRSPGVCV	PAAEHLRREI	540																						
QY	541	LAKFLHLM	MSYVYVELLRSFFYVTETTFQKNRLF	FFYRKSVMKLSQSIGIQHLKRVOLRE	600																								
DB	541	LAKFLHLM	MSYVYVELLRSFFYVTETTFQKNRLF	FFYRKSVMKLSQSIGIQHLKRVOLRE	600																								
QY	601	LSEAEVQHRREAR	PALLTSRLRFTPKPDGLRPI	VNMDYVVGARTFRREKRAERLTSRVKA	660																								
DB	601	LSEAEVQHRREAR	PALLTSRLRFTPKPDGLRPI	VNMDYVVGARTFRREKRAERLTSRVKA	660																								
QY	661	LFSVLNTERAR	PGLLGASVLGLDDIHRWRTFVLR	RAODPPPELYFVKVDVTGAYDTI	720																								

Db 661 LFSVLNTERARRPGLGASVGLDDIHRAMTFFVLVRQAOPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLQPYMQFVAHL 780
Db 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLQPYMQFVAHL 780
Qy 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOQSILSTL 840
Db 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOQSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLLVDDFLLVTPHLTHAKTFLRTIVRGVPEYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLRLLVDDFLLVTPHLTHAKTFLRTIVRGVPEYGCVVNL 900
Qy 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNSIQTVCTNIIKLLLOAVRFHACVLQLP 1020
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNSIQTVCTNIIKLLLOAVRFHACVLQLP 1020
Qy 1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFL 1080
Db 1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFL 1080
Qy 1081 KLTRHRYVYPLGLSLTAQTLQSRKLP GTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTRHRYVYPLGLSLTAQTLQSRKLP GTTLTALAAANPALPSDFKTILD 1132

RESULT 3

US-09-843-676-225
; Sequence 225, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-09-843-676-225

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWFLVQGDPAAPRALVAQCLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWFLVQGDPAAPRALVAQCLVCVPM 60
Qy 61 DARPPAAPSPROVSCUKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPEAFTTSVR 120
Db 61 DARPPAAPSPROVSCUKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPEAFTTSVR 120
Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLGCGERANVHVSREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCGERANVHVSREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
Qy 241 GAAPERTPVGGSWAHPCGTRGSPDRGFCVSPARPABEATSLEGALSGTRSHPSVG 300
Db 241 GAAPERTPVGGSWAHPCGTRGSPDRGFCVSPARPABEATSLEGALSGTRSHPSVG 300
Qy 301 RQHAGPPSTSRPPRPMWDTFCPPVYAEIKHFLYSSGDKQLRPSFLSSLSRSLTGARRL 360
Db 301 RQHAGPPSTSRPPRPMWDTFCPPVYAEIKHFLYSSGDKQLRPSFLSSLSRSLTGARRL 360
Qy 361 VETIFLGSRPWMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLEAAVT 420
Db 361 VETIFLGSRPWMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLEAAVT 420
Qy 421 PAAGVCAREKPGQSWAAPEBEDTDPRLVOLLRHSSPQWQVYGFVRACTLRCLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPEBEDTDPRLVOLLRHSSPQWQVYGFVRACTLRCLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKKFISLGKHAKLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKKFISLGKHAKLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKPLHMLMSVYVVELLRSFFYVTTTFOKNRLLFFYKSKSVMSKQSLQSGIRQHLKRVQLE 600
Db 541 LAKPLHMLMSVYVVELLRSFFYVTTTFOKNRLLFFYKSKSVMSKQSLQSGIRQHLKRVQLE 600
Qy 601 LSEAEVQREARPAALTSRLRFPKPDGLRPIVNMNDYVVGARTFREKRAERTLSRVKA 660
Db 601 LSEAEVQREARPAALTSRLRFPKPDGLRPIVNMNDYVVGARTFREKRAERTLSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVGLDDIHRAMTFFVLVRQAOPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVGLDDIHRAMTFFVLVRQAOPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLQPYMQFVAHL 780
Db 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLQPYMQFVAHL 780
Qy 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOQSILSTL 840
Db 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOQSILSTL 840

QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDLFLVTPHLLTHAKTFLRLLVGRGPEYGCNVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLLRLVDLFLVTPHLLTHAKTFLRLLVGRGPEYGCNVNL 900
QY 901 RKTVVNFVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOQSDYSYARTSIRASLTFF 960
Db 901 RKTVVNFVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOQSDYSYARTSIRASLTFF 960
QY 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Db 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
QY 1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAFLL 1080
Db 1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAFLL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQTOLSRKLPQTTLTLEAAANPALPSDFKTIID 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQTOLSRKLPQTTLTLEAAANPALPSDFKTIID 1132

RESULT 4

US-09-953-052-2
; Sequence 2, Application US/09953052
; Patent No. US20020173476A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997

; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-003600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPCRAVRSLLRSHYREVLPATFVRRLLPGQGWRLVQRGDPAAFRALVAQCLVCVPM 60
Db 1 MPRAPCRAVRSLLRSHYREVLPATFVRRLLPGQGWRLVQRGDPAAFRALVAQCLVCVPM 60
QY 61 DARPPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDGCARGCPPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDGCARGCPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALPVLVAPSCAYVCGPPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALPVLVAPSCAYVCGPPPLYQLGA 180
QY 181 ATQARPPPHASPRRLGCERAWNSHREAGVPLGAPGARRRGGSASRSLPKRPRR 240
Db 181 ATQARPPPHASPRRLGCERAWNSHREAGVPLGAPGARRRGGSASRSLPKRPRR 240
QY 241 GAAPEPERTVQGSWAHPGRTGRPSDRGFCVVSPPARPAEEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPERTVQGSWAHPGRTGRPSDRGFCVVSPPARPAEEATSLEGALSGTRHSHPSVG 300
QY 301 ROHAGPPSTSRPPRMDTPCPVVAETKHFLYSSGDKLEQLPSPFLSLRSLTGARRL 360
Db 301 ROHAGPPSTSRPPRMDTPCPVVAETKHFLYSSGDKLEQLPSPFLSLRSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSPPQVYGVFVRACLRLLVPFGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSPPQVYGVFVRACLRLLVPFGLMGS 480
QY 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCGVCPAAEHLRBEI 540
Db 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCGVCPAAEHLRBEI 540
QY 541 LAKFLHMLMSVYVVELLSRFFVYVTTTQKRLFFYKSVMSKLSQSIGIRHLLKRVQJRE 600
Db 541 LAKFLHMLMSVYVVELLSRFFVYVTTTQKRLFFYKSVMSKLSQSIGIRHLLKRVQJRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWTFLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWTFLVRVAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PQDRLTEVIASTIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/053,758
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 225:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1132 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-053-758-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRAVRSLLRSHYREVLPLATEFVRLPGQWRLVQRGDPAAPRALVAQCLVCPW 60
Db 1 MPRAPCRAVRSLLRSHYREVLPLATEFVRLPGQWRLVQRGDPAAPRALVAQCLVCPW 60

Qy 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLVQLGA 180
Db 121 SYLPNTVTDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLVQLGA 180

Qy 181 ATQARPPPHASGRRRLRCERANVHVSREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240
Db 181 ATQARPPPHASGRRRLRCERANVHVSREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240

Qy 241 GAPEPRTVPGQSWAHPGTRGSDRGFCVSPAPAEATSLGALSGRTRHSPSVG 300
Db 241 GAPEPRTVPGQSWAHPGTRGSDRGFCVSPAPAEATSLGALSGRTRHSPSVG 300

Qy 301 ROHHAGPPTSRRPMDTCCPPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARLL 360
Db 301 ROHHAGPPTSRRPMDTCCPPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARLL 360

Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420

Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRQHSSPWQVYGVFVRACLRLRLLVPPGLWGS 480

Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRQHSSPWQVYGVFVRACLRLRLLVPPGLWGS 480
Qy 481 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAARHRLREEI 540
Db 481 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAARHRLREEI 540
Qy 541 LAKFLHMLMSVYVVELLRSFYVTEFTFQKNRLFYFVRKSVWSKLQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHMLMSVYVVELLRSFYVTEFTFQKNRLFYFVRKSVWSKLQSIGIRQHLKRVQLRE 600
Qy 601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRAQDPPPELYFKVDVGTAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRAQDPPPELYFKVDVGTAYDTI 720
Qy 721 PDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCCGIPQGSILSTL 840
Db 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCCGIPQGSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLLVTHPLTHAKTFLRTLVRGVPBGCVNVL 900
Db 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLLVTHPLTHAKTFLRTLVRGVPBGCVNVL 900
Qy 901 RKTVMNFPVEDEALGATFVQMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGATFVQMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960
Qy 961 NRGFKAGRNMRRLFGVLRKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db 961 NRGFKAGRNMRRLFGVLRKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Qy 1021 FHQVWKNTFFFLRVISDTASLCYILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
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Qy 1081 KLTRHRVTYVPLLSLRTAQTOLSRKLPGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLLSLRTAQTOLSRKLPGTTLTALAAANPALPSDFKTILD 1132

RESULT 7
US-10-208-243-2
; Sequence 2, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-208-243-2

Query Match		100.0%;	Score 5961;	DB 14;	Length 1132;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1132;		Conservative	0;	Mismatches	0;
			Indels	0;	Gaps
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLLGPGQWRLVORGDPAAFRALVAQCLVCVPW	60	
Db	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLLGPGQWRLVORGDPAAFRALVAQCLVCVPW	60	
Qy	61	DARPPPAAPSFRQVSCLEKELVARVLQRL	CERGAKNVLAFFGPFALLDGGARGGPEAFTTSVR	120	
Db	61	DARPPPAAPSFRQVSCLEKELVARVLQRL	CERGAKNVLAFFGPFALLDGGARGGPEAFTTSVR	120	
Qy	121	SYLNTVTDALRGSGAWGLLRVGDVLLRHLL	ARCALFVLVAPSCAYQVCGPPLYQLGA	180	
Db	121	SYLNTVTDALRGSGAWGLLRVGDVLLRHLL	ARCALFVLVAPSCAYQVCGPPLYQLGA	180	
Qy	181	ATQARPPPHASGPRRLRCERAWHNSVREAC	VPGLPAPGARRRGGSGASRSLPLPKPRR	240	
Db	181	ATQARPPPHASGPRRLRCERAWHNSVREAC	VPGLPAPGARRRGGSGASRSLPLPKPRR	240	
Qy	241	GAAPPERTPVQGSWAHPGRTRGSDRGFCV	SPARPAEBATSLLEGALSGTRHSHPSVG	300	
Db	241	GAAPPERTPVQGSWAHPGRTRGSDRGFCV	SPARPAEBATSLLEGALSGTRHSHPSVG	300	
Qy	301	RQHAGPPSTSRPPRPWDTPCPVYAETKHP	LYSSGKEQLRPSFLSSLRPSLTGARRL	360	
Db	301	RQHAGPPSTSRPPRPWDTPCPVYAETKHP	LYSSGKEQLRPSFLSSLRPSLTGARRL	360	
Qy	361	VETIFLGSRPWMPGTPRRLPRLPORVMQMR	PLFTLELGNHAQCPGVLLKTHCPRAAVT	420	
Db	361	VETIFLGSRPWMPGTPRRLPRLPORVMQMR	PLFTLELGNHAQCPGVLLKTHCPRAAVT	420	
Qy	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVQL	LROHSSPWQYGVFVRACLRLRLVPPGLWGS	480	
Db	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVQL	LROHSSPWQYGVFVRACLRLRLVPPGLWGS	480	
Qy	481	RHNERRFLNTKFTISLGKHAKLSLOELTW	QMSVRDCAWLRRSPGVGCVPAAEHRLREEI	540	
Db	481	RHNERRFLNTKFTISLGKHAKLSLOELTW	QMSVRDCAWLRRSPGVGCVPAAEHRLREEI	540	
Qy	541	LAKFLHLMVSVVVELLRSFFVTETTFQKNR	LEFFYRKSVMKLSQSIGIROLKRVOLRE	600	
Db	541	LAKFLHLMVSVVVELLRSFFVTETTFQKNR	LEFFYRKSVMKLSQSIGIROLKRVOLRE	600	
Qy	601	LSEAEVRQREARPAALLTSRLRFIPKPDGL	RPINMDDYVVGARTFRREKRAERLTSRVKA	660	
Db	601	LSEAEVRQREARPAALLTSRLRFIPKPDGL	RPINMDDYVVGARTFRREKRAERLTSRVKA	660	
Qy	661	LFSVLNTERARRPGLLGASVLGLDDIHRAW	TFVLVRAQDPPPELYFVKVDVTGAYDTI	720	
Db	661	LFSVLNTERARRPGLLGASVLGLDDIHRAW	TFVLVRAQDPPPELYFVKVDVTGAYDTI	720	
Qy	721	PODLRLTEVIAIIIPQNTYCYRRYAVVQKA	AHGHVRKAFKSHVSTLTDLPYMQFVAHL	780	
Db	721	PODLRLTEVIAIIIPQNTYCYRRYAVVQKA	AHGHVRKAFKSHVSTLTDLPYMQFVAHL	780	
Qy	781	QETSPLRDVAVIEOSSLINEASSGLFDVFL	FMCHHAVIRGKSVVOCQIPQGSILSTL	840	
Db	781	QETSPLRDVAVIEOSSLINEASSGLFDVFL	FMCHHAVIRGKSVVOCQIPQGSILSTL	840	
Qy	841	LCSLCYGDMENKLFAGIRRDGLLLRLVDD	FLVLVTPHLLTHAKTFLRTLVRGVPYGCVVNL	900	
Db	841	LCSLCYGDMENKLFAGIRRDGLLLRLVDD	FLVLVTPHLLTHAKTFLRTLVRGVPYGCVVNL	900	
Qy	901	RKTVMNPFVEALGGTAFVQMPAHGLFPW	CGLLDTRTLEBVQSDYSYARTSIRASLTFF	960	
Db	901	RKTVMNPFVEALGGTAFVQMPAHGLFPW	CGLLDTRTLEBVQSDYSYARTSIRASLTFF	960	
Qy	961	NRGFKAGNMRKLFVGLRLKCHSLFDLDQ	VNSLQTVCTNLYKILLQAYRFHACVLQLP	1020	
Db	961	NRGFKAGNMRKLFVGLRLKCHSLFDLDQ	VNSLQTVCTNLYKILLQAYRFHACVLQLP	1020	
Qy	1021	FHQQVKNPTFFLRVISDTASLCYSILKAK	NAGMSLGAKGAAGPLPSEAVQWLCHQAPLL	1080	

Db	1021	FHQQVKNPTFFLRVISDTASLCYSILKAK	NAGMSLGAKGAAGPLPSEAVQWLCHQAPLL	1080	
Qy	1081	KLTRHRYVYVPLLGSLRFTAQTLQSRKLP	GGTTLTALEAAANPALPSDFKTIID	1132	
Db	1081	KLTRHRYVYVPLLGSLRFTAQTLQSRKLP	GGTTLTALEAAANPALPSDFKTIID	1132	
RESULT 8					
US-10-054-295-225					
; Sequence 225, Application US/10054295					
; Publication No. US20030044953A1					
; GENERAL INFORMATION:					
; APPLICANT: Cech, Thomas R.					
; Lignner, Joachim					
; Nakamura, Toru					
; Chapman, Karen B.					
; Morin, Gregg B.					
; Harley, Calvin					
; Andrews, William H.					
; TITLE OF INVENTION: No. US20030044953A1el Telomerase					
; NUMBER OF SEQUENCES: 225					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Townsend and Townsend and Crew LLP					
; STREET: Two Embarcadero Center, 8th Floor					
; CITY: San Francisco					
; STATE: California					
; COUNTRY: United States of America					
; ZIP: 94111					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/10/054,295					
; FILING DATE: 18-Jan-2002					
; CLASSIFICATION DATA:					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: 08/854,050					
; FILING DATE: <Unknown>					
; APPLICATION NUMBER: US 08/846,017					
; FILING DATE: 25-APR-1997					
; APPLICATION NUMBER: US 08/844,419					
; FILING DATE: 18-APR-1997					
; APPLICATION NUMBER: US 08/724,643					
; FILING DATE: 01-OCT-1996					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Apple, Randolph T.					
; REGISTRATION NUMBER: 36,429					
; REFERENCE/DOCKET NUMBER: 015389-002930US					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (415) 576-0200					
; TELEFAX: (415) 576-0300					
; INFORMATION FOR SEQ ID NO: 225:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 1132 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; MOLECULE TYPE: protein					
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:					
US-10-054-295-225					
Query Match					
Best Local Similarity 100.0%; Score 5961; DB 14; Length 1132;					
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	PLATEVRRLLGPGQWRLVORGDPAAFRALVAQCLVCVPW	60	
Db	1	MPRAPRCRAVRSLLRSHYREVLP	PLATEVRRLLGPGQWRLVORGDPAAFRALVAQCLVCVPW	60	
Qy	61	DARPPPAAPSFRQVSCLEKELVARVLQRL	CERGAKNVLAFFGPFALLDGGARGGPEAFTTSVR	120	

Db 61 DARPPAAPSPRQVSCUKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRLCGERAMNHSVREAGVPLGLPAGARRGGGSASRSLPLPKRPRR 240
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Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPAPABEATSEALSGTRHSHPSVG 300
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Qy 301 ROHAGAPSTSRPPMDTPCPCPVYAKTHFLYSBGDEQLRPSFLLSLSLRPSLTGARRL 360
Db 301 ROHAGAPSTSRPPMDTPCPCPVYAKTHFLYSBGDEQLRPSFLLSLSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRPLPQRYWQMRPLFELILGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRPLPQRYWQMRPLFELILGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREPQGSVAAPBEEDTPRLVOLLROHSSFPWQYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREPQGSVAAPBEEDTPRLVOLLROHSSFPWQYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERRFLNNTKPFISLGKHAQSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRREEI 540
Db 481 RHNERRFLNNTKPFISLGKHAQSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRREEI 540
Qy 541 LAKEFLHLMSSVYVELLRSFFYVETTFQKNRFFFYRKSWSKLQSIGIRQHLKRVQLRE 600
Db 541 LAKEFLHLMSSVYVELLRSFFYVETTFQKNRFFFYRKSWSKLQSIGIRQHLKRVQLRE 600
Qy 601 LSEAEVQREARPALITSRLFTPKPDGLRPIVNMDDYVVGATFRREKAEALTSRVKA 660
Db 601 LSEAEVQREARPALITSRLFTPKPDGLRPIVNMDDYVVGATFRREKAEALTSRVKA 660
Qy 661 LFSVLNVERARRPGLGASVLGDDIHRWRTFVLRVRAODPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLGASVLGDDIHRWRTFVLRVRAODPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PQDLTEVIAIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDAVVEQSSLINEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSIILSTL 840
Db 781 QETSPLRDAVVEQSSLINEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSIILSTL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLILRLVDDFLVTPHLTHAKTFLRTLVRGPVPGCVNVL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLILRLVDDFLVTPHLTHAKTFLRTLVRGPVPGCVNVL 900
Qy 901 RKTWNPPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOSSDYSSVARTSIRASLTF 960
Db 901 RKTWNPPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOSSDYSSVARTSIRASLTF 960
Qy 961 NRQFKAGNRNRKLFGLVRLKCHSLFLDLQVNSLQVCTNIYKILLQAVRFHACVLQLP 1020
Db 961 NRQFKAGNRNRKLFGLVRLKCHSLFLDLQVNSLQVCTNIYKILLQAVRFHACVLQLP 1020
Qy 1021 FHOQVKNPFFLRVISTDASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWILCHQAFLL 1080
Db 1021 FHOQVKNPFFLRVISTDASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWILCHQAFLL 1080
Qy 1081 KLTRHRVTVYVPLLGSLTAQTQLSRKLPGTTTLTALEAAANPALPSPDKTILD 1132
Db 1081 KLTRHRVTVYVPLLGSLTAQTQLSRKLPGTTTLTALEAAANPALPSPDKTILD 1132

RESULT 9

US-10-054-611-225

; Sequence 225, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-611-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MPAPRCRAVRSLRSHREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPAAPSPRQVSCUKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPRQVSCUKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRLCGERAMNHSVREAGVPLGLPAGARRGGGSASRSLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRRLCGERAMNHSVREAGVPLGLPAGARRGGGSASRSLPLPKRPRR 240

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Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRHSHPVG 300
Db 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRHSHPVG 300
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Qy 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRFLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRFLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPOGSVAAPBEEDTDPRRLVQLLRQHSPPWQYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSVAAPBEEDTDPRRLVQLLRQHSPPWQYGFVRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKCFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKCFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLE 600
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLE 600
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Db 601 LSEAEVQHRREARPAALLTSRLRFTPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPQYMRQFVAHL 780
Db 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPQYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCQGIPOGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCQGIPOGSILSTL 840
Qy 841 LCSLCYGD MENKLFAGTRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGD MENKLFAGTRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTVVNFVEDEALGCTAFVQMPAHGLFPWCGLLDTLTLEQSDYSYARTSIRASLT 960
Db 901 RKTVVNFVEDEALGCTAFVQMPAHGLFPWCGLLDTLTLEQSDYSYARTSIRASLT 960
Qy 961 NRGFKAGNMRRKLFVLRKCHSLFLDLQVNSLQTVCTNITYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVLRKCHSLFLDLQVNSLQTVCTNITYKILLQAYRFHACVLQLP 1020
Qy 1021 FHOQWKNPTFFLRVISTASICYSLKAKNAGSLGAKGAGPLPSEAVOWLCHQAFLL 1080
Db 1021 FHOQWKNPTFFLRVISTASICYSLKAKNAGSLGAKGAGPLPSEAVOWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLP GTTLTAL EAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLP GTTLTAL EAAANPALPSDFKTILD 1132
RESULT 10
US-10-105-963-2
; Sequence 2, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; TITLE OF INVENTION: Recombination
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; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-963-2
Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRLPGQGRVLVQGDPAAPRALVAOCLVCVPW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRLPGQGRVLVQGDPAAPRALVAOCLVCVPW 60
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Db 61 DARPPPAAPSFROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPPPAFTTSVR 120
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Qy 181 ATOARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240
Db 181 ATOARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240
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Db 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRFLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPOGSVAAPBEEDTDPRRLVQLLRQHSPPWQYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSVAAPBEEDTDPRRLVQLLRQHSPPWQYGFVRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKCFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKCFISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLE 600
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLE 600
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Db 601 LSEAEVQHRREARPAALLTSRLRFTPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPQYMRQFVAHL 780
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Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCQGIPOGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCQGIPOGSILSTL 840
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QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNNL 900
Db LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNNL 900
QY 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLDLRTLLEVQSDYSYARTSIRASLTFF 960
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QY 961 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Db NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
QY 1021 FHQQWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db FHQQWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTRHRVTYVLLGSLRTAQQLSRKLP GTTTLTALBAAANPALPSDFKTILD 1132
Db KLTRHRVTYVLLGSLRTAQQLSRKLP GTTTLTALBAAANPALPSDFKTILD 1132
RESULT 11
US-10-044-692-2
; Sequence 2, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-692-2
Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVQRGDPAAFRALVAOCLVCVPW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVQRGDPAAFRALVAOCLVCVPW 60
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Db 61 DARPPPAAPSFQVSCLEKELVARVQLQRCERGAKNVLAFGFALLDCARGGPEAFTTSVR 120
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Db 301 ROHHAGPPSTSPRRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRLRSLTCARLL 360
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QY 481 RHNERRFLRNTKFIISLGHAKLSLOELTKMSVDRDCAWLRSPGVCGVPAAEHRLREI 540
Db 481 RHNERRFLRNTKFIISLGHAKLSLOELTKMSVDRDCAWLRSPGVCGVPAAEHRLREI 540
QY 541 LAKFLHLMMSVYVVELLSRFFVYVTTTTFQKNRLFYRKSVWSKLSQSIGIRQHLKRVOLRE 600
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QY 601 LSEAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKAEERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKAEERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFYKVDVTGAYDTI 720
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QY 721 PDRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVKAFKSHVSTLTLDLPYMRQFVAHL 780
Db 721 PDRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVKAFKSHVSTLTLDLPYMRQFVAHL 780
QY 781 QETSPLRDAVJIEQSSSLNEASSGLFDVPLRPMCHHVAIRGKSVYQCGIPQGSILSTL 840
Db 781 QETSPLRDAVJIEQSSSLNEASSGLFDVPLRPMCHHVAIRGKSVYQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNNL 900
Db 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNNL 900
QY 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLDLRTLLEVQSDYSYARTSIRASLTFF 960

Db 901 RKTUVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDLTDRTLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
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Qy 1081 KLTRHRVTVYVLLGSLRTAQOLSRKLPCTTLTALAAAAANPALPSDFKTIILD 1132
Db 1081 KLTRHRVTVYVLLGSLRTAQOLSRKLPCTTLTALAAAAANPALPSDFKTIILD 1132
RESULT 12
US-10-044-539-2
; Sequence 2, Application US/10044539
; Publication No. US2003010093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 19-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-539-2
Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRLRPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRLRPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPPAAPRQVSCIKELVARVLQRLCERGAKNVLAFGPALLDARGGPPAEFTTSVR 120
Db 61 DARPPPAAPRQVSCIKELVARVLQRLCERGAKNVLAFGPALLDARGGPPAEFTTSVR 120
Qy 121 SYLPTNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLPTNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Qy 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLKPRRR 240
Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLKPRRR 240
Qy 241 GAAPERTPTVQGSWAHPGRTGRGFCVSPARPABEATSLEGALSCTRSHSPSVG 300
Db 241 GAAPERTPTVQGSWAHPGRTGRGFCVSPARPABEATSLEGALSCTRSHSPSVG 300
Qy 301 RQHAGPSTSRPRPMDTPCPVYAKTKHFLYSSGDKQOLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVYAKTKHFLYSSGDKQOLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPWMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPYVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPYVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSPPWQYGFVRACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSPPWQYGFVRACLRRLVPPGLMGS 480
Qy 481 RHNERRFLRNTKFPISLGKHAJLSQELTWKMSVRDCAWLRPSRGVCGVPAAEHRLREI 540
Db 481 RHNERRFLRNTKFPISLGKHAJLSQELTWKMSVRDCAWLRPSRGVCGVPAAEHRLREI 540
Qy 541 LAKEFLHMLMSVYVVELLRSFFYVTETTFQKNRLFYYRKSVMWSKLQSIGIRQHLKRVQRE 600
Db 541 LAKEFLHMLMSVYVVELLRSFFYVTETTFQKNRLFYYRKSVMWSKLQSIGIRQHLKRVQRE 600
Qy 601 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADQPPPELVKDYVTGAVDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADQPPPELVKDYVTGAVDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QETSPLRDAVVEIOSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSII STL 840
Db 781 QETSPLRDAVVEIOSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSII STL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPH LTHAKTFLTRVGVPEVGCVVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPH LTHAKTFLTRVGVPEVGCVVNL 900
Qy 901 RKTUVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDLTDRTLEVSQSDYSYARTSIRASLTF 960
Db 901 RKTUVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDLTDRTLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

Db 961 NRGFAGNRMRRLKFGVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAVRHACVLQLP 1020
Qy 1021 FHQVWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWMLCHQAFLL 1080
Db 1021 FHQVWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWMLCHQAFLL 1080
Qy 1081 KLTRHRVTVYVLLGSLRTAQQLSRKLPFGTTLTAAEAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVYVLLGSLRTAQQLSRKLPFGTTLTAAEAANPALPSDFKTILD 1132
RESULT 13
US-10-295-681-57
; Sequence 57, Application US/10295681
; Publication No. US20030166270A1
; GENERAL INFORMATION:
; APPLICANT: E. Premkumar Reddy
; APPLICANT: Sushil G. Rane
; APPLICANT: Richard V. Mettius
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REVERSIBLY
; TITLE OF INVENTION: INDUCING CONTINUAL GROWTH IN NORMAL CELLS
; FILE REFERENCE: 6056-307
; CURRENT APPLICATION NUMBER: US/10/295.681
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/334,760
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-681-57

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRVRSLRSHYREVLPATFVRRLGPGWRLVORGDPAAFRALVAQCLVCVPV 60
Db 1 MPRAPCRVRSLRSHYREVLPATFVRRLGPGWRLVORGDPAAFRALVAQCLVCVPV 60
Qy 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGANGLLRRVGGDDVLVHLLARCAALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGANGLLRRVGGDDVLVHLLARCAALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATOARPPHAGPERRRIGCERAMNHSVREAGVPLGLPAGARRGGGSASRLPLKPRR 240
Db 181 ATOARPPHAGPERRRIGCERAMNHSVREAGVPLGLPAGARRGGGSASRLPLKPRR 240
Qy 241 GAAPEPERTVQGSWAHPGRTGSDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPERTVQGSWAHPGRTGSDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300
Qy 301 RQHAGPPSTSRPPRPWDTPCPVYATKHFVYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPRPWDTPCPVYATKHFVYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGRSPPMCTPRLRLPQRYWQMRPLFLELGNHQAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGRSPPMCTPRLRLPQRYWQMRPLFLELGNHQAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEBEDTDPRRLVQLLRHSSPMQVYFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEBEDTDPRRLVQLLRHSSPMQVYFVRACLRRLVPPGLWGS 480
Qy 481 RHNERRLRNTKPFISLGKHAJLSQBLTWKMSVRDCAWLRRSPGVGCVPAASHRLREEI 540
Db 481 RHNERRLRNTKPFISLGKHAJLSQBLTWKMSVRDCAWLRRSPGVGCVPAASHRLREEI 540

Qy 541 LAKFLHMLSVYVVELLSFFVYVTTTFOKNRLEFFYRKSVMKSLQSTIGIRHQLKRVOLRE 600
Db 541 LAKFLHMLSVYVVELLSFFVYVTTTFOKNRLEFFYRKSVMKSLQSTIGIRHQLKRVOLRE 600
Qy 601 LSAEVRQREARPPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSAEVRQREARPPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRPFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRPFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PQDRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDADVIEQSSSLNEASSGLFDFLRFMCHHAVIRGKSYVQCQIPQSSILSTL 840
Db 781 QETSPLRDADVIEQSSSLNEASSGLFDFLRFMCHHAVIRGKSYVQCQIPQSSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVNL 900
Qy 901 RKTIVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTLRTLEVOSDYSSVARTSIRASLTF 960
Db 901 RKTIVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTLRTLEVOSDYSSVARTSIRASLTF 960
Qy 961 NRGFAGNRMRRLKFGVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAVRHACVLQLP 1020
Db 961 NRGFAGNRMRRLKFGVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAVRHACVLQLP 1020
Qy 1021 FHQVWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWMLCHQAFLL 1080
Db 1021 FHQVWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWMLCHQAFLL 1080
Qy 1081 KLTRHRVTVYVLLGSLRTAQQLSRKLPCTTTLTAAEAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVYVLLGSLRTAQQLSRKLPCTTTLTAAEAANPALPSDFKTILD 1132

RESULT 14

US-10-325-810-2
; Sequence 2, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/325,810
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-325-810-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAARALVAQCVCVPW 60
DB 1 MPRAPCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAARALVAQCVCVPW 60
QY 61 DARPPAAPSPROVSCLELVARVLQRLCERGANVLAFAFGFALLDARGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPROVSCLELVARVLQRLCERGANVLAFAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLPTVTDALRGSGANGLLRLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTVTDALRGSGANGLLRLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPHAGPRRRLGCEAMNHSVREAGVPLGLPAGNRRGGSGASRLPLPKPRR 240
DB 181 ATQARPPHAGPRRRLGCEAMNHSVREAGVPLGLPAGNRRGGSGASRLPLPKPRR 240
QY 241 GAAPEPRTPVQGSWAHPGRTGSDRGFCVSPARPABEATSGALSGTRHSHPSVG 300
DB 241 GAAPEPRTPVQGSWAHPGRTGSDRGFCVSPARPABEATSGALSGTRHSHPSVG 300
QY 301 RQHAGPPSTSRPPMDTPCPVYAETHKFLYSSGDKQLRPSFLSSLRPSITGARRL 360
DB 301 RQHAGPPSTSRPPMDTPCPVYAETHKFLYSSGDKQLRPSFLSSLRPSITGARRL 360
QY 361 VETIFLGSRPMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCPCYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRPMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCPCYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLRQHSFPWQYGVFVRACLRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLRQHSFPWQYGVFVRACLRLVPPGLWGS 480
QY 481 RHNERRFLRNTKKFISLGKHAKLSQLBETWKMVSVDCAWLRRSPGVCVPAAEHRLREI 540

DB 481 RHNERRFLRNTKKFISLGKHAKLSQLBETWKMVSVDCAWLRRSPGVCVPAAEHRLREI 540
QY 541 LAKFLHLMVSVYVVELLRSPFYVTETTFQKNRFFFYKSVKMSKLSQSIGIRHKLKVOLRE 600
DB 541 LAKFLHLMVSVYVVELLRSPFYVTETTFQKNRFFFYKSVKMSKLSQSIGIRHKLKVOLRE 600
QY 601 LSEAEVRQHREARPALITSRLRPIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPALITSRLRPIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNVERARRRGLLGASVLGLDDTHRAWRTEFLVRADDPPELYFVKVDVTGADTI 720
DB 661 LFSVLNVERARRRGLLGASVLGLDDTHRAWRTEFLVRADDPPELYFVKVDVTGADTI 720
QY 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRPMCHHVRIRGKSVYVQCQGIPOGSI LSTL 840
DB 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRPMCHHVRIRGKSVYVQCQGIPOGSI LSTL 840
QY 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCYNL 900
DB 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCYNL 900
QY 901 RKTVMNPPVEDEALGGTAFVQMPAHGLFPMCGLLLDTRTLEVDSDSYARTSIRASLTF 960
DB 901 RKTVMNPPVEDEALGGTAFVQMPAHGLFPMCGLLLDTRTLEVDSDSYARTSIRASLTF 960
QY 961 NRGFKAGRNRRKLFGLRLKCHSLFDLQVNSLQVTCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFKAGRNRRKLFGLRLKCHSLFDLQVNSLQVTCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTRHRVTVYVPLLSGLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTVYVPLLSGLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132

RESULT 15
US-10-388-578-2
; Sequence 2, Application US/10388578
; Publication No. US2003022441A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence
; APPLICANT: Geron Corporation
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; APPLICANT: Shelton, Dawne
; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of H
; TITLE OF INVENTION: Embryonic Stem Cells
; FILE REFERENCE: 135/001
; CURRENT APPLICATION NUMBER: US/10/388,578
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Custom
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-388-578-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:23:35 ; Search time 50 Seconds
(without alignment)
2178.348 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSDFKTILD 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: P1r1.*
2: P1r2.*
3: P1r3.*
4: P1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	T03844	telomerase catalyt
2	724.5	12.2	1123	T51517	telomerase reverse
3	594.5	10.0	989	T03838	telomerase catalyt
4	395	6.6	1132	T31107	telomerase reverse
5	363	6.1	1117	T14891	telomerase IEC 2.7
6	356.5	6.0	884	S53396	telomerase catalyt
7	176.5	3.0	3530	A59266	unconventional myo
8	172.5	2.9	660	Q0BE3	BHLF1 protein - hu
9	144	2.4	3511	A59295	unconventional myo
10	142.5	2.4	1560	T00080	hypothetical prote
11	140.5	2.4	1892	T18314	hypothetical prote
12	140	2.3	1460	1 EDBE1F	immediate-early pr
13	139.5	2.3	552	T75311	ABC transporter, A
14	138.5	2.3	924	S27923	gene LF3 protein -
15	135	2.3	1356	1 C45219	N-methyl-D-asparta
16	134.5	2.3	946	T07810	inositol 1,4,5-tri
17	134	2.2	606	TG7302	orotidine 5'-phosp
18	133	2.2	1106	J00405	hypothetical 119.5
19	132	2.2	860	S55543	RNA-directed DNA p
20	131.5	2.2	1184	TG01763	atrophin-1 - human
21	131	2.2	1446	1 A45344	immediate-early pr
22	130.5	2.2	1184	T S05082	atrophin-1 - human
23	130.5	2.2	2715	T13049	eyelid - fruit fly
24	129.5	2.2	383	S32975	gene BCR2 protein
25	129	2.2	403	S2796	prpL2 protein - hu
26	129	2.2	1776	TG86280	protein T5E21.13 [
27	128.5	2.2	628	S01955	hypothetical prote
28	128	2.1	376	T75580	adenine deaminase-
29	127.5	2.1	1048	T31425	C-terminal domain-

30	127	2.1	260	2	S22373	proline-rich prote
31	127	2.1	505	2	S72273	actin-depolymerizi
32	127	2.1	580	2	T43481	probable mucin DKF
33	127	2.1	847	1	A53800	mixed-lineage prot
34	127	2.1	862	2	T46289	hypothetical prote
35	127	2.1	1039	2	T35878	hypothetical prote
36	126.5	2.1	603	2	H75272	probable nucleic a
37	126	2.1	330	2	E98119	transposase, uncha
38	125.5	2.1	1067	2	T18196	pol protein - silk
39	125.5	2.1	574	2	T43556	Wiskott-Aldrich sy
40	125.5	2.1	574	2	T38819	wiskott-aldrich sy
41	125	2.1	522	2	S52216	viral proteinase -
42	125	2.1	1914	2	T42635	tenascin Y precurs
43	124	2.1	1298	1	EDB775	immediate-early pr
44	124	2.1	1323	2	S27224	N-methyl-D-asparta
45	123.5	2.1	381	2	S16506	hypothetical prote

ALIGNMENTS

RESULT 1

T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03844
P:Matsumura, T.M.; Marin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
Science 277, 955-959, 1997
A:Title: telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: Z15111; MUID:97400623; PMID:9252327
A:Accession: T03844
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NAK>
A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g
A:Experimental source: kidney
C:Genetics:
A:Gene: TRT
A:Map position: 5p

Query Match		100.0%;	Score 5961;	DB 2;	Length 1132;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1132;		Conservative	0;	Mismatches	0;
		Indels	0;	Gaps	0;
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	1	MPRAPRCRAVRSLLRSHYREVLP	1
Db	1	MPRAPRCRAVRSLLRSHYREVLP	1	MPRAPRCRAVRSLLRSHYREVLP	1
Qy	61	DARPPPAAPSFROVSCLEKELVARVLQRLCERGA	61	DARPPPAAPSFROVSCLEKELVARVLQRLCERGA	61
Db	61	DARPPPAAPSFROVSCLEKELVARVLQRLCERGA	61	DARPPPAAPSFROVSCLEKELVARVLQRLCERGA	61
Qy	121	SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCA	121	SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCA	121
Db	121	SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCA	121	SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCA	121
Qy	181	ATQARPPPHASGPRRRRLGCRANVHSVREAGVPLG	181	ATQARPPPHASGPRRRRLGCRANVHSVREAGVPLG	181
Db	181	ATQARPPPHASGPRRRRLGCRANVHSVREAGVPLG	181	ATQARPPPHASGPRRRRLGCRANVHSVREAGVPLG	181
Qy	241	GAAPERTPVGGSGMAHPGTRGSPDRGFCVVS	241	GAAPERTPVGGSGMAHPGTRGSPDRGFCVVS	241
Db	241	GAAPERTPVGGSGMAHPGTRGSPDRGFCVVS	241	GAAPERTPVGGSGMAHPGTRGSPDRGFCVVS	241
Qy	301	QOHAGPPSTSRPRPMDTCCPPVYATKHFLYSSGDK	301	QOHAGPPSTSRPRPMDTCCPPVYATKHFLYSSGDK	301
Db	301	QOHAGPPSTSRPRPMDTCCPPVYATKHFLYSSGDK	301	QOHAGPPSTSRPRPMDTCCPPVYATKHFLYSSGDK	301
Qy	361	VETIFGSRPMPGTPRRRLPRLPORYWQMRPLFLEL	361	VETIFGSRPMPGTPRRRLPRLPORYWQMRPLFLEL	361
Db	361	VETIFGSRPMPGTPRRRLPRLPORYWQMRPLFLEL	361	VETIFGSRPMPGTPRRRLPRLPORYWQMRPLFLEL	361

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QY 421 PAAGVCAREKPGSSVAAPEEDTDPRRLVQLLRQSSPMQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGSSVAAPEEDTDPRRLVQLLRQSSPMQVYGFVRACLRRLVPPGLWGS 480
QY 481 RNNRRPLNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCPVAAEHLREEI 540
Db 481 RNNRRPLNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCPVAAEHLREEI 540
QY 541 LAKFLHLMMSVVVWELLRSFFVTETTFQKNLFFYRKSVMSKQSIGIROHLKRVQRE 600
Db 541 LAKFLHLMMSVVVWELLRSFFVTETTFQKNLFFYRKSVMSKQSIGIROHLKRVQRE 600
QY 601 LSEAEVRQHREARPALLTSRLFIKPKDGLRPIVNMVYVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPALLTSRLFIKPKDGLRPIVNMVYVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNREARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNREARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVRRYAVVOKAAHGVKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKQNTYCVRRYAVVOKAAHGVKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPLRDAVIEQSSSNEASSGLFDVFLRFMCHHAVRIRGKSYVOCQIGIPQGSILSTL 840
Db 781 QETSPLRDAVIEQSSSNEASSGLFDVFLRFMCHHAVRIRGKSYVOCQIGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLRVDDFLVPLTHAKTFTLTVRGVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLRVDDFLVPLTHAKTFTLTVRGVPEYGCVVNL 900
QY 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDRTLLEVOQSDYSYARTSIRASLTF 960
Db 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDRTLLEVOQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNMRRKLFVULRKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVULRKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
QY 1021 PHQQWKNPTFPLRVIDSTASLCYSILKAKNAGSLGAKGNAAGPLSEAVOMLCHOAFLL 1080
Db 1021 PHQQWKNPTFPLRVIDSTASLCYSILKAKNAGSLGAKGNAAGPLSEAVOMLCHOAFLL 1080
QY 1081 KLTHRVTVYPLLGSLRTAQTSRKLPGTTLTALEAANAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVYPLLGSLRTAQTSRKLPGTTLTALEAANAANPALPSDFKTILD 1132

RESULT 2
telomerase reverse transcriptase - Arabidopsis thaliana
N;Alternate names: protein F5E19_190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51517
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; New
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Accession: T51517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1123 <SAT>
A;Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A;Experimental source: cultivar Columbia; BAC clone F5E19
C;Genetics:
A;Map position: 5
A;Introns: 100/3; 125/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A;Note: F5E19_190

Query Match 12.2%; Score 724.5; DB 2; Length 1123;
Best Local Similarity 23.8%; Pred. No. 3.2e-41;
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Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;
QY 1 MPRAPRCRVRSLRSHYREVLPATFV-----RRIGPQCWR-----L 38
Db 1 MPAPRHRVRPEILLWRLFGRNARNLDAIVDLINRNIIQPEQCRGCGCLGSSDKPAFL 60
QY 39 VQRGDDPAAFALVAQCLVCVPWDARPPPAAPSFRQVSCCLKELVARVLRL---CERGAKN 95
Db 61 LRSDDPPIHYKLLHRFCV-VLHEQTPLDLDFSTWMSQREIIVERIEMQSGCD--CQN 117
QY 96 VLAFFGALLDARGGGPEAFTTSVRSYLPTVNTDALRGSGAMGLLHRRVGDVVLHLLAR 155
Db 118 VICARYDKYDQS-----SPILELLT-SSSWEFLKRVGHVDMVYLLQQ 159
QY 156 CALFVLVAPSCAYQVCGPPLYQLGAAT-----QARPPPHASGPRRRRLGCERAWNHSVR 209
Db 160 TSIFLPLGKHKQVSGPPLCIKHKTLSVHENKRRDDNVQPTTKRWLSSAVDDCPKD 219
QY 210 AGVPLGLPAG---ARRRGGSSASRLPLPKPRRGA-----APEPERTVPGGWSA 257
Db 220 DSATI--TPIVGEDVDQHREKTKTKRSIYLYKRRRKQKYNFKKVCNACITP----- 271
QY 258 HPGTRGPSDRGFCVVSPARPAEAEATSLGALSQTRHSHPSVGRQHHAGPSTSRPRPW 317
Db 272 ---STNGKVSTG-----NDENLHIGINGSITDFVKQAKQ----- 303
QY 318 DTPCPPVYAEWKFLYS--SGDKELRPSFLLSLRPSLTGARRLVETIFLGRPMMPGTP 376
Db 304 -----VKRNKNFKFGLSETYSVIPPNHILKTLRPNCSDSLKLMNHIFGEVNVWSTPS 356
QY 377 RRLPLRPQ---RYQWRPLFLELLGNHACQPGVLLKTHCP-----LBAATPAAG 424
Db 357 HGKNGCPSSICLYHSLLKSLKXKLGKTKYSHLKMLLDKHCHVLLQEDALSGTSSOSS 416
QY 425 VCAREK-----POGSVAA-----PEEDTDPRRLVQLLRQSSPMQVYGFVRACLRRLVPPG 476
Db 417 --RRQKADKLPHGSSSSQTKPKCPSVEERKL-----YCTNDQVVSFIWALCRVIVES 468
QY 477 LWSGRHNERFRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCPVAAEHL 536
Db 469 LGTTTHQWRVURKNIAWVSRRRNBKCTVQNQFLHKVPKSDPFFFAKKE--LCCMVNNGHEL 526
QY 537 REE-----ILAKFLHLMMSVVVWELLRSFFVTETTFQKNLFFYRKSVMSKQSIG 588
Db 527 QSESIRSTQOMLCTKWISWLFLEIVKLVHNFVFATESQGGRLNIYYIRKSWERLISKE 586
QY 589 IRQHLKRVQLRELSAEVVRQHREARPALLTSRLRPIKPDGLRPIVNMVYVGARTFRRE 648
Db 587 ISKALDGYVLVDAAEASSRKK-----LSKFRFLPKANGVRMVLID-----FSSS 630
QY 649 KRAERLTSRVKALPSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPP-PELY 707
Db 631 SRQSGL-----RDTTHAVLKDIOIKKEPFDVLGSSVFDHDDFYRLNCLPYLIHLRSQSGELPPLY 686
QY 708 FVKVDVTGAYDTIPQDRLTEVIASIIKQNTYCVRRYAVVOKAAHGH-----VRKAFKS 761
Db 687 FVADVAFKAFSDVQGLLHVIVQFLKDB--YILNRCCLVCCGKRSWVWVWILVSSDKNS 744
QY 762 HVSTLTDLOPYMRQFVAHLQETSPLRDAVIEQSSSNEASSGLFDVFLRFMCHHAVIR 821
Db 745 NPSRFTSTVPYNA-----LQ-----SIVVDKGENHRVRKKDLMMVITGNKMLKNMLQLD 792
QY 822 GKSYYVQCQIGIPQGSILSTLCLSCYGMENKLPAGI-----RRDGL----- 862
Db 793 KSFVQIAGIPQGHRLSSLLCCFYGHLETLIYPIFLEEASKOVSSKECSREELIPTS 852
QY 863 --LRLVDDFLVTPHITHAKTFTLTVRGVPEYGCVVNLKRTVNVNFEVDE----- 912
Db 853 YKLLRFDDVLFVSTSRDQASSFVRLKHKGFQKVCNCFMNETKFCINFEDKEHRCSNRM 912
QY 913 --ALGGTAFVQMPAHGLFPWCGLLLDRTLLEVOQSDYSYARTSIRASLTNRGFKAGNM 970
Db 913 FVGDNVGFVFR-----WTGLLINRTEFVQVDYTRYLSGHSISSTFSFVAMQKNKVRNL 964
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Query Match
Best Local Similarity 6.6%; Score 395; DB 2; Length 1132;
Matches 136; Conservative 114; Mismatches 305; Indels 58; Gaps 15;

QY 450 QLLRQHSSPMQVGVFVRACLRRLVPCLGWSRRNERRFLNTKKFTSLGHAKLSQELT 509
DB 451 QLFEYQQDQRQIQINFLTETEVANFPKPNFLEGG-KKKIFNNKKMLQFKVFRPFESFTISLL 509
QY 510 WKMSVRDCAWLRRSPGCVCPAAEH---RLREBILAKFLHLMMSVVVELLRFYVVTET 566
DB 510 NKPRVNEVSWL-----SFKCKDENKKCFMNEHEHFVKLVKWVFEDLAITLMRCFYISTEK 565
QY 567 TFOKNRLFYRKVSWMKSIGIRHLKRVLSELSEAEVRQHRARPALLTSRURFIPIK 626
DB 566 AKEQRIIFYRKNIWNWIRLSIDDLKQ-NLKQVEKKEMRIFCESQ-NFAFGKLRLIPIK 623
QY 627 PDGLRPVNMVYVGARTFRRE-----KRAERLTSRVK--ALFSVLNYEARRPGLLG 677
DB 624 GTDFRPIM-----TFNRKIIPNQGVKFQSRMTTNKKLQTAHMMLKXKSKMPKHSGF 674
QY 678 ASVLGDDITHRAWRTFVLVRAQDPPELYFKVDVTVGAYDTIPQDRLTEVIAS----- 731
DB 675 FAVENVDDIMKYENFVQWK-QINSPKUYFVAMDIEXCYDNVCERVNFVFNQKSDLMDK 733
QY 732 -----IIKQNTVYVRYYAVQKAAGHVRYKAFKSHVSTLTLDLPVMRQFVAHQBT 783
DB 734 EYFILNTFVLKRNKNNIIVERSNFRKLPIKOYPYKFKQ-IGIDGSYPTLPFILEDEFND 792
QY 784 SPLRDADVIEQSSLINEASSGLFDVFLPWCCHYAIRGKSVYQCQIPQGSILTLLCS 843
DB 793 LNMKETIIVEOQRKKFPKNDLLQPVLKICQNYYTFNKKQYKQMKGPQGLCYSYILLSS 852
QY 844 LCYGDWENKLFAGIRRD-----GLLLRVDDFLVTPHTLTHAKTFLRTLVRGVPEY 894
DB 853 FYIANLENALQLFRKESMDPEKPENILMLRLTDYLLMTTEKNAMLFIKYLQSLGN 912
QY 895 GCNVNLRTVNVFFVEDSALGTAPVQ--MPAHGLFWPCGLLLDTRLLEVQDSYSSVAR 951
DB 913 FFKFHMKLKTNFALNLQIKICTNTYTQIDSINDDLFWIGISIDIKTLNTIQNI-NITK 971
QY 952 TSIRASLTFNGRGKAGRNMRKLFGLVLKCHSLFDLDQVNSLQTCTNIYKILLQAYR 1011
DB 972 EGILCTLNANNQTNESILWLWKKLKSFLMNNISPVFKSTINTKQFANITLSKLIYAEEK 1031
QY 1012 FHACVLQLP-FHQ 1023
DB 1032 YVACCQEFKRFHE 1044

RESULT 5
Tl4891
telomerase (EC 2.7.7.-) catalytic chain p133 - Tetrahymena thermophila
N:Alternate names: telomerase reverse transcriptase
C:Species: Tetrahymena thermophila
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Tl4891
R:Collins, K.; Gandhi, L.
Proc. Natl. Acad. Sci. U.S.A. 95, 8485-8490, 1998
A>Title: The reverse transcriptase component of the Tetrahymena telomerase ribonucleoprotein complex
A:Reference number: Z18252; PMID:98337941; PMID:9671704
A:Accession: Tl4891
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1117 <COL>
A:Cross-references: UNIPROT:O77448; EMBL:AF061284; NID:g3335166; PID:g3335167; PIDs:AAC3
C:Genetic: A
A:Gene: TERT
A:Genetic code: SGCS
C:Keywords: nucleotidylyltransferase

R;Du, Z.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of *S. cerevisiae* cosmid 8543.
A;Reference number: S53390
A;Accession: S53396
A;Molecule type: DNA
A;Residues: 1-884 <DUZ>
A;Cross-references: UNIPROT:Q06163; EMBL:U20618; NID:g2258165; PID:g662136; GSPDB:GNO001
A;Experimental source: strain S288C (AB972)
C;Genetics:
A;Gene: SGD:YLR318w
A;Cross-references: SGD:S0004310; MIPS:YLR318w
A;Map position: 12R

Query Match	6.0%;	Score 356.5;	DB 2;	Length 884;
Best Local Similarity	22.1%;	Pred. No. 3.1e-16;		
Matches 167;	Conservative 127;	Mismatches 309;		
Indels 151;	Gaps 28;			

329	Qy	KHFLYSSGDKEQURAPS--FLLSSURPSLITGARRLV---ETIFLGRSPWMPGTPRRRLRPLP	383
185	Db	QKFLH-----KLNINSSSFFPYSKILPSSSSIKKLTDLREAF-------PTNLVKIP	230
384	Qy	QRYQWQREPLFLE-LLGNHAQCPGVLLKTHCPLRAAVTPAAGVCAREKPGQSVAAPEED	442
231	Db	QRUKVRINLTQKLLKHKRLNYSIILNSICP-----PUBGTVL-----	269
443	Qy	TDPRRLVQLLRQHSSPWQVYGFVRACLRRLRVPGLWGRSHNRERFLRNTKKFISLGHKAK	502
270	Db	-----DLSHLSRQ--SPKSERLVKFIIIVLIQKLLPOEMFGSKKNKGKIIKNLNLLSLPLNGY	324
503	Qy	LSLQELTWKMSVRDCAMLRKSPGCVGVPAAEHLRL--EEILAKFLHMLMSVYVVELLRSP	566
325	Db	LPFDSLKKLRLKDFRWL-----FISDWFTKHNFENLNQLAICISWLFQROLIPKIIQTF	380
561	Qy	FYVETITFQXNRLFFYFKSVMSKLSIGIQHLKRVQLRELSEAEV--RQHREARPALLT-	618
381	Db	FYCTEIS-STVTIVYFRHDTWKNLITPFI VEYFKTY-----LVENNVCRNHNSYTLSPFNH	435
619	Qy	SLRLFIKPKDGLRLIVNMYYV-----GARTFRREKRAERLTSRVKALFSVLNVERARR	672
436	Db	SKMRIIPKKS-----NNEPRIIAIPCRGADEBEFTIYKENHKNAIQPTOKILEVLRNKR	489
673	Qy	PGLLGASVLGLDDIHRARWTFVLRV--RAQDPPPELYFVKVDVTGAVDTPQDRLTEVIA	730
490	Db	PTSF-TKISYPTQIADRIKBFQKRLKKFNVLPELYFMKFDVKSCYDSIPRMECMRILK	548
731	Qy	SLIKPONTYCVRRYAVVQKAAGHVRAFKSHVSTLTDLOPYMQQFVAHLQETSPLRDAV	790
549	Db	DALKNENGFFVRSQYFN--TNTGVULKF-NNVNASRVPRPY-----EL	589
791	Qy	VIEQSSLSNEASSGLFDVFLRFMCHHVARIRGSKSYVOCGIIPQGSIIISTLLCSLCYGDW-	849
590	Db	YIDNVRTVHLSNQDVINNVEMEIPKTAIWLVEDKCYIREDLGFGSSLSAPIVDLVYDLL	649
850	Qy	--ENKLPAGIRRDGLLRLVDDFLVTPHLTHAKFTLTVRGVPEYGCVVNLBKTV-VN	906
650	Db	EYSEFKASPSQDTLILKLADDFLIIISTDQQOVINIKKLAGMGFPQKYNKANRDKILAVS	709
907	Qy	FPVEDEALGGTAFVQMPAHGLFPMWGLLDDTRTLEVSQDYSYSA RTSIRASLTNRGPKA	966
710	Db	SQSDDDT-----VIFQCAHII FVKELEVWKHSMTWNFHRS-----KS	748
967	Qy	GRNMRRKLFGLRLKCHSLFLDLQVNSLQTVCTNI-----YK-----ILLQA	1009
749	Db	SKGIFRSLIALENTRISYKTIIDTNLSTNTVLMQIDHWVKNI SECYKSAFKDLSINTQN	808
1010	Qy	YRHFACVLQJPFPHQOVWQNPFFFLRVISDTSALC	1043
809	Db	MQFH-----SFLQRIIEMTWVSGC	826

RESULT 7
A59266

unconventional myosin-15 - human
C/Species: Homo sapiens (man)
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: A59266
R/Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Man, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A/Title: Characterization of the human and mouse unconventional myosin XV genes responds
A/Reference number: A59266; MUID:20021762; PMID:10552926
A/Accession: A59266
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-3530 <LIA>
A/Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:G6224682; PIDN:AAF05903.1; PID:962
F:1225-1887/Domain: myosin motor domain homology <NMO>

Query Match	3.0%	Score 176.5;	DB 2;	Length 3530;
Best Local Similarity	20.6%;	Pred. No. 0.0041;		
Matches	263;	Conservative 144;	Mismatches 392;	Indels 475; Gaps 68;
Qy	107	ARGGPPPEAFITSS-----VRSYLP-----NTVTDALRGSGAWG	138	
Db	2313	SRGGPKVFGNSWDSDEDMSTRPQOEHPMKVILDGYSYSHNQDGTNGETEAQGT-ATH	2371	
Qy	139	LLLRVRGDDVLVHLLARCALFVLVAP-----SCAYQVCQPPILYQLGAA-----	181	
Db	2372	QESDSLGEPAVPKHGLDCLYLSLFDPVLSYGDADLEKPTAIAYRMKGQPGGGSSSGTE	2431	
Qy	182	-TQARP--PHASGPRRLGCBRAWNHSVREAGV--PLGLPAGARRGGSGAS-RSLP	233	
Db	2432	DTRRRPEPEKPIGLDASTLALQAETH--KQVLLARGMTLQATLQQOQLPAAALRSLP	2489	
Qy	234	LPKRRRGAAPERTPVGGGSAHPRGTRGSPDRGFCVVSPARPAEEATSEGALSGR	293	
Db	2490	AEXPP-----APEAQPTSVGTGPPAKPVILR-----ATPKPLAPA-----	2524	
Qy	294	HSHPSVGRQHAGPSTSRPPRPWDTCPPVYA-----ETKHFLSYSGDKQLRPSFLL	347	
Db	2525	-----PLAKAPRLPIKPAAPVLAQDOASPET-----TSPSELVRYSTLN	2565	
Qy	348	SSLRPSLTGARRLVETIFLGSRRPWPQTGTRPRLPQRYWQMP-----LFLELLGNH	400	
Db	2566	SEHFPOPT--QQIKNIVRQVQFRCGRPEALRKDGKVFMKRPDPHEEALMLKQMTH	2623	
Qy	401	AQCFYG-----VLLK--THCPLRAAFTPAAAGVCAREKPGQGSVAAPPE-EDTPRRLV	449	
Db	2624	LAAPGPTQVSREAVALVKPVTSA-P-RPSMAPTSAL-----PSRSLPEPELTQTRLHRLI	2677	
Qy	450	--QLLRQHSPPWOYGFVR-----ACLR-----RL	472	
Db	2678	NPNFYGYQDAPWKI--FLRKEVFYPKDSYHPVQLDLLFRQILHDTLSEACLRISEDRL	2735	
Qy	473	VPPLGWSRHNRERRFLRNTKFFISLG-KIAKLSLQBLTWKMSVDCAWLRRSPGVGCVPA	531	
Db	2736	RMKALFAQNO-----LDTQKPLVTESVKRAVSTARDTWEV-----YFSRIPATGSVGT	2785	
Qy	532	AEHLRBEELIAFLHLMMSVYVELLR-----SFFYVTTTF-OKNR	572	
Db	2786	G-----VQLLA-----VSHVGITKLRLWKVGGQAGQLRVLRAYSFADILFTMPSONM	2834	
Qy	573	LPFYKRSVMSKLOSIGIRHKLKRVQLRELSAERVQHRARPALLTSRLRFIPKPDGLRP	632	
Db	2835	LENFLAS--EKVILFSARAH-----QVKTLVDDDFILBLKK-----	2867	
Qy	633	IVNMDYVVGARTPRRKRKAERLTSRVKALFSLVNLRYER-----RRPGLLGAS-----	679	
Db	2868	--DSDYVVAVRNLPEDPA-----LLAFHKGDIIHLQLEPPRPGVYSAGCVVR	2913	
Qy	680	--VLGLDDIHR-----AWRTFVLVRQAQDPPPELYFVKVDVTGAYD-----TTP-QDRLT	726	
Db	2914	RKVYILEEURLRRGPDFGWRPGTITHGRVRFPSL-----VQPAASAPDFLOLTFEPGGRAA	2869	
Qy	727	EVIASIIKPNQTYCVRRY-----AVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHLQ	781	

20

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Db 2970 AVAAVASAAAAQEVRRREGPPVRRASADHGEDALALPPY-TMLEFAQKYFRDPQRRPQ 3028
QY 782 E-----TSLRDVAIVIOSSSLNEASSGLDFVFLRFMCHHAVR 819
Db 3029 DGLRLSKSPRSRTLEDMLCTKTKPLQSLIELSDSSLSKXWATDMFLAVRMFGDAPLK 3088
QY 820 IRKSVVOCGIPQGSILSTLCSLCYGD---MENKLFAGI-----RRDG 861
Db 3089 GOSDLDLVLCN-----LLKLC-GDHEVWRDECYQVVKQITDNTSSKQSCQGW 3136
QY 862 LLLRLVDDF-----LLVTPHLTHAKTFLRLVR--GVPEYG---CVNLRKTVVNFVVED 911
Db 3137 RLIIYIVTAVHSCSEVLHPLHTR---FLODVSRTPGLPFQGIKACEQNQKTL----- 3186
QY 912 EALGGTAFVQMPAHGLFPMCGLLDTRTLEQSDVSSVARTSIRASLTFNRFAGRNMR 971
Db 3187 -RFGG-----RLEUPSS-----IELRAML-----AGRSSK 3210
QY 972 RKLK-----GV---LRKCHSLFLDLQVNSLQTVCT-----NIYKILLQAYRPHA 1014
Db 3211 RQLFLPLGGLERHLKIKTKTVALDV---VEEICAEMALTRPEAFNEVIFVVTNRQGV 3266
QY 1015 CVL-----QLPFHQQVWKQPTFF-----LRVISTASLCY 1044
Db 3267 CPLSRRAVLDAVSEMEQVGGYMLWFRRLVMDQPLKFENELYVTMHNQVLPDYLKGLF 3326
QY 1045 SILKAKNAGMSILGKAAGPLPSEAVQWLCHQAFLLKLTTRHVT---YVPLGLSLRTAQ- 1100
Db 3327 SSVPASR-----PSEQ---LLOQVSKLASLQHRKADHYFLP---SVREQE 3366
QY 1101 ---TQLSRKLPGTT 1111
Db 3367 YIPALQVYRTTAGST 3380

RESULT 8
QBHE3
BHLF1 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C:Accession: A03742
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrall, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A>Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Accession: A03742
A:Molecule type: DNA
A:Residues: 1-660 <BAN>
A:Cross-references: UNIPROT:P03181
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A>Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667; PMID:6087149
A:Contents: annotation: protein coding region
C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 2.9%; Score 172.5; DB 1; Length 660;
Best Local Similarity 26.1%; Pred. No. 0.00078;
Matches 94; Conservative 16; Mismatches 159; Indels 91; Gaps 16;
QY 167 AYQVC-GPPYLQGAATQ--RPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGAR 222
Db 244 AAQRCFAGPPPTTRSGAAQRTTHRRPPGCPRSARNPGCPRTWR---RRSGAQRGHPPPGAG 300
QY 223 RRGGSASRLP-LPKPRRGAPEP-ERTPVGGSWAHQPTRGSDRGFCV-VSPAR-- 277
Db 301 QRPSTGGRPAAPGAPGTPAAPGGGAAPVSGATPHPERGSGPADPAAARLPFERQE 360
QY 278 -----PABEATISLEGAL-----SGTRHSHP 297
Db 361 PRLPDOLAAQRCFAGPPPTTRSGAAQRTTHRRPPGCPRSARNPGCPRTWRRRSGAQRGHP 420
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QY 298 SVGRQHAGPPSTSRPRPW--DTPC-----VYAEKHFLYSSGDK-----QLR 342
Db 421 PPGAGQRPSTGTRGPAAPGAPGTPAAPGGGAAPVSGATPHPERGSGPADPAAARLP 480
QY 343 PSFLLSLRSLTGARRLVETIFLGRPWMPG-----TPRRLRLPQ-----RYQM 389
Db 481 PERQEPRLPDOLAAQRCP-----AGPPPTTRSGAAQRTTHRRPPGCPRSARNPGCPRTWR 536
QY 390 RPLFLELLGNHQAOCFYGLLKTHCPL--RAAVTPAAGVCAREKPGQSGVAAPBEDTDRR 447
Db 537 RS-----GAQRGHPFGAGRPSTGTRGPAAPGATPAAAPGGGAAPVSGATPHPER 591

RESULT 9
A59295
unconventional myosin-15 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59295
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probat, F.J.; Barber, T.D.; M;
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A>Title: Characterization of the human and mouse unconventional myosin XV genes response
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Accession: A59295
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3511 <LIA>
A:Cross-references: UNIPROT:Q9QZ24; GB:AF144095; NID:g6224684; PIDN:AAF05904.1; PID:g62
C:Genetics:
A:Gene: MGI:Myo15
A:Cross-references: MGI:1261811
A:Map position: 11:33.9
F:1209-1871/Domain: myosin motor domain homology <MMO>

Query Match 2.4%; Score 144; DB 2; Length 3511;
Best Local Similarity 17.6%; Pred. No. 0.68;
Matches 189; Conservative 117; Mismatches 385; Indels 380; Gaps 44;
QY 3 RAPRCRAVRSLLRSHYREVLPPLATFVRLGPGQWRLVQRGDPAAPRALVALVACLVCVP-- 59
Db 677 RPPRLASPVGSLRQH-----PPW-----AAAHVFFPPQA 707
QY 60 --WDARPPAA-----PSFQVSCCLKELVARVLCRCERGAKNVLAFGA 102
Db 708 NWMGFAEPPTGTSPEVAPDLLAPPVPRPSFR-----ASRSRSRRAAYGFP 751
QY 103 LLDGARGGPPPEAFTTSVRSYLPNTVTD--ALRGGAGWGLLLRRVGDVVLHLLARCALFV 160
Db 752 -----SPSLIGSRRRPHLPSPQSLRSLPGQG----- 778
QY 161 LVAPSCAVQVCPPYLQGAATQARPPPHASGPPRRRLGCERAMNHSVREAGVPLG----- 215
Db 779 -----YHSPGLPLSPQLSLRGGFPQFPFPPPPRRPQSLREAF--SLRRASRGLGPPRSP 830
QY 216 -----LPACGARRRGSGASRSLPKR-----PRGGAAPPERT--PVQGS 255
Db 831 VLGSFRPPSPPLLKHGFRHRSNLPLSLPRTWRRLSEPPTRAVKPWVHRAYPPPSAGP 890
QY 256 WAHPGRTRGSDRGFCVVSAPPAEATSLGALSGTRHSHPSVGRQHAGPPSTSRPR 315
Db 891 W---GASTGALE-----QENQREADESETPTWTPPLAPSWVDVMDPTQRPSS 935
QY 316 PWDTPC-----PPVYAEKHFLYSS-----GDKEQLRPSFLS 348
Db 936 FWPEGIGSLRGFRPPPPVPENPLEHTSPSCPEQSDRVSNLTGIFLGQHHDFCGQLTK 995
QY 349 SLRPSLTGARRLVETIFLGRPWMPGTFRRL-PRLPQRYWQMRPLFLELGNH----- 400
Db 996 SADSPL---EKPEVTVLGD-POPFAPEALNTPFNKNVSVSRKVLRLSASYPLVTCQ 1051
QY 401 --AQCP-----YGVLLKTHCPLRAAVTPAAGVCAREKPGQS----- 434
```

Db 1052 ARATWQWHRWKTTSRTAPLAPTRAPGQLLKAGEQPRAEPRFAVVMQVQVGVSSFRPK 1111
QY 435 ---VAAPDEEDTDPR-----LVQLRQHSPPWQVGVFRAC 468
Db 1112 GPAPVQPEHFDQDEQAPQACSLRWPCLPWPTDAHCLMSRINTYSSQSHLRGHGDC 1171
QY 469 LRL---VPPGLWGRHNRFLRNTKKFI SLGKHAKLSLOELTWKMSVRDCAMLRSPG 525
Db 1172 HKSLWKTRPQSW---QNKMSIRNLPMSRREQHREDGVEDMTQLEDLQETTILAN--- 1225
QY 526 VCVPAAEHLREELAKFL-----HMLMSVVVELLRSP-----FVYT 564
Db 1226 ---LKTRFERNLIYTIIGILSVNPNYRFAIYGPQVQVQSGRALGPNPHLFAIA 1279
QY 565 ETTFOK-----NRLFFYR-----KSVSKL-----QSIGIROLKRVOLRELSE 603
Db 1280 NLAFAKMLDAKQNCQVVISGSGSKTEATKLLRCLAMNQRRDVMQIKILEATPLLE 1339
QY 604 A-----EVROHREARPALLTSLRFLPKPDGLRPVNMVYVVGARTFREKRAER----- 653
Db 1340 AFGNAKTVRNDSSR---FGKRVFEIFLEGVCIGAITSOYLLEKSRIVFQAKNERNYHIF 1396
QY 654 -----LTSRVKALFSLNZE-----RARRPGLLGASVLGLDDIHRARWTFVLVRAQD 701
Db 1397 YELLAGLPAQLRQAFSLQEAETYYLNLQNGNCEIAGKS--DADDPR----- 1441
QY 702 PPELYFYKVDVGTAYDITIPDRLTEVIASIIKPNQTVCVRYAVVQKAAHGHVRKAPKS 761
Db 1442 -----LLAAMEVLG--FTSEDDQSTFRILASIIHLGNVFEKHETDAQEVA----- 1485
QY 762 HVSTLTDLPYMRQFVAHLQETSP--LRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819
Db 1486 SWSAREIQ-----VAELLQVSPBGLQAKTEKVTETIRE-----KIFPLTVESAVD 1534
QY 820 IRGKSYVOCQIPOGSIILSTLCSLCYGDMEKLPAGI--RRDGLLLRLVD 868
Db 1535 AR-----DAIAKVALYLLFGWLITRVALNSPKQDTLSAILD 1572

RESULT 10
T00080
hypotheical protein KIA0522 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00080
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
A:Reference number: Z14086; MUID:98290545; PMID:9628581
A:Accession: T00080
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1560 <NAG>
A:Cross-references: UNIPROT:060275; EMBL:AB011094; NID:g3043567; PIDN:BAA25448.1; PID:g3
A:Experimental source: brain; clone HGI393
C:Genetics:
A:Note: KIA0522

Query Match 2.4%; Score 142.5; DB 2; Length 1560;
Best Local Similarity 29.5%; Pred. No. 0.28;
Matches 65; Conservative 15; Mismatches 89; Indels 51; Gaps 12;

QY 173 PPLYOLGAATQARPPHAGSPRRRLGCERANHSVREAGVP-----LGLPAGARRRG 226
Db 1365 PPLPOLGSI-----PPPPASAP--PVGPHR---HFFAHGVPFGPQHYTLGRGPRAPRGAG 1415
QY 227 SASRSLPLPKRP--RRGAPEPERTPVGQSWAHPGTRGSDRGFCVVSVPARPAEATSL 285
Db 1416 GHPQFAPHGRPLHQTSPLYSFAPQHPAH---KQGPKHFISSHHPQMPAAGAGG 1472
QY 286 EGAL--SGTRHSHPSVGRQHGAGPPSTSR---PPRPWDTPCPPVVAETKHF----- 331

Db 1473 PGSRPPGGSYSHP-----HHQPSLSPHSPPIPHPSYPPPLPPPSHTPHSPLPTSPHGP 1527
QY 332 LYSQDEQRLRPSFLSLSRSLTGCARRLVETIFLGRSPW 371
Db 1528 LHASGPPAQPTTP--VQTPRPSQA-----GSAPW 1554

RESULT 11
T18314
hypotheical protein L7610.4 - Leishmania major
C:Species: Leishmania major
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18314
R:Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18876
A:Accession: T18314
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1892 <OLI>
A:Cross-references: UNIPROT:097007; EMBL:AL034356; NID:e1371878; PID:e1371559; PIDN:CAV
C:Genetics:
A:Note: L7610.4

Query Match 2.4%; Score 140.5; DB 2; Length 1892;
Best Local Similarity 23.4%; Pred. No. 0.51;
Matches 111; Conservative 47; Mismatches 195; Indels 121; Gaps 25;

QY 44 PAAPRALVAQCLVCVPWDARPPPAAPSRQVSCIKELVARVLQRLCERGAKNVLAFGAL 103
Db 366 PSSLHPQOQPVIVLVP---QRPAPQOERLPRLYSTTRPAGPSRGAVQNNIYAGMAA 422
QY 104 LDGARGGPPBEAFTSVRS-----YLPNTVTDALRGSGAWGLLRVGVDDVLVHLLARCAL 158
Db 423 EDTSSGASEVTSTSSRTRQVFRAPVTASDPTGS--PYGAM-----PT 465
QY 159 FVLVAPSCAYQVCGPLYQVGAATQARPPPHASG-----PRRLGC-----ERAWN 204
Db 466 YAVVMPQ--RSLPAPPKTGASAGLPPSPAPAAEQPOHNSRCPSPSSRSPQESRD 523
QY 205 HSVREAGVPLGLPAGAR-----RRGSASRSLP-----LPKRP--RRGAPEPERT 249
Db 524 HAAREQ--PLPQPPQKRPALPORHQRAETAKSQLPPRMRLPADFPYSEELIPEQRR-- 580
QY 250 PVGQSWAHPGTRGSDR--GFCVVSVPARPA-----BEATLEGALSGTRHSHP--SVGRQ 302
Db 581 ---EGADGNASTQSGHRGHSVTVSQOQLSLSHBEDLSLMSLSATVAAPISTKTD 637
QY 303 HHAGPPSTSRPPRPMWDTPCPPVYAETKHFVLYSSGDKQLRPSFLLSLRPSLTGARRL-V 361
Db 638 PYAGHTAPDGEPRPLHVPMPPIIQRP---YAATEE-----GAPFSV 678
QY 362 ETIFLGRPWWGTTPRLPLRPLQRYWQMRPLFLELGNHQAOCYV--VLLKTHCPLRAA-- 418
Db 679 RKVTAPQESDAPSPRSHSP-----PAEHTLLSHRGAADAGEAAAKEETREQLSAK 728
QY 419 ---VTPAAGVCAREKQ-----GSVAAPAEEDTDPRRLVQ---LLRQHSSP 458
Db 729 EAVTAMTAGVQSSKKFQQLQHEPDGS---PNGDDVD--ELLEADDLLIMQSRP 777

RESULT 12
EDBEIF
immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
C:Species: suid herpesvirus 1
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713
A:Molecule type: DNA

A;Residues: 1-1460 <CHE>
A;Cross-references: UNIPROT:P111675
C;Superfamily: herpesvirus immediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 2.3%; Score 140; DB 1; Length 1460;
Best Local Similarity 24.3%; Pred.No. 0.38;
Matches 114; Conservative 35; Mismatches 163; Indels 158; Gaps 27;

QY 46 AFRALVAQCILCVCPWDARPPAPAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLD 105
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
704 ACRGVLERLLPC-PLRLPARAPALGPAACLEVTAAALL-----ALRD 746
QY 106 GARG-GPPE-----AFTTSYRSYLPTNTVDALRGSGAWGLLLRRVGDDVLVHLLAR 155
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
747 AIFGAGPAERQQAADSVALVARTVAPLVRYSDGARAREAAW-----TYA 791
QY 156 CALFVLVAPCAVQVCPPYQLGAATQARPPIPHASPRRLGCERAWN-----S 206
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
792 AALF---APA--NVAGARL-----AEAAARPGPAEPAP-----GLPLPWPEQGLVWPAPA 837
QY 207 VRAGVPLGIAPAG-----ARRRGSSARSFLPKRPGRGAAPPERTPVCGGSWAHPGRT 262
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
838 PAAAGAPSGLPGGPSPATKSGSTKSSTSGTSGLSGSS-----GYARLP RRR 887
QY 263 RGPSSDRGFCVVSP-----ARP--AEETATSLEG-ALSCTRHSHPVGRQHAGAPPSTGRP-- 313
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
888 PGFSARAQAEEAPRAGARRPDGEEDGLSGSALRGDGCHRD--DEEDGPRRKERSLG 945
QY 314 --PRPWDTPCPPVYAETHKFLYSGDKELQRPFLSSLRPSLTGARRLVETIFLGSRPW 371
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
946 LGAP- DPAPALVSSSSS--SSSSDDRLLR-----RP-----LGMPE 980
QY 372 MPCTPRRLPLQRYQMRLPLELLGNHAQCYPVLLKTHCP-----L 415
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
981 HPADGGFRVPAG-----ETHTRPSAALAAYCPFEVARALVDOEVFPFLW 1028
QY 416 RAAVT--PA--AGVCAREKPGSWAAPEDTDPRRLVQLLRQSHSPWOV 461
DB 1029 RPALTDPDAALAHIAAR--RGAAGP-----LRRRAWMRIADPEDV 1069

RESULT 13
F75311
ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75311
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036996; PMID:10567266
A;Accession: F75311
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-552 <WHI>
A;Cross-references: UNIPROT:Q9RS9H; GB:AE002048; GB:AE000513; NID:g6459929; PIDN:AAF1168
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2145
A;Map position: 1

Query Match 2.3%; Score 139.5; DB 2; Length 552;
Best Local Similarity 22.3%; Pred.No. 0.11;
Matches 134; Conservative 38; Mismatches 196; Indels 233; Gaps 27;

QY 132 RGSGAWGLLLRRVGDDVLVHLLARCALFVLVAP-----SCAQVQCGP 173
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
24 RGS---RLQFRVSGKSTRIRFTSTSLFCULPLGUTIASSTGSTFHSSDVAAAPR 80
QY 174 P----LYQLGAATQARPPPHASGPRRLRG-----C 199


```
QY 338 KEQLRPSFLSSRLTGARRLVETIFLGSRRWMPG-TPR-RL-PRLPQRYWQMRPLFL 394
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 EPRTR-----LQPATPRRSGAADPADPVGHAPRAPGPEPRTRLQPATPRRSGAADP--A 235
QY 395 ELLGNHAQCPCYGVLLKTHCPLRAAVTPAAGVCAREKPGSGSVAAPDEEDTDPRRLVQ 450
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
236 DPVG-HPAAPRAPGPEPRTRLQPATPRRSGAADPADPVGHAPRAPGPEPRTRLQ 290

RESULT 15
C45219
N-methyl-D-aspartate receptor chain NMDAR2D-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: C45219
R:Ishii, T.; Moriyoishi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa
J. Biol. Chem. 268, 2836-2843, 1993
A:Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor
A:Reference number: A45219; MUID:93155102; PMID:8428958
A:Accession: C45219
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1356 <ISH>
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:124264)
C:Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
F:451-879/Domain: glutamate receptor homology <GRH>

Query Match 2.3%; Score 135; DB 1; Length 1356;
Best Local Similarity 27.2%; Pred. No. 0.76;
Matches 88; Conservative 16; Mismatches 102; Indels 118; Gaps 22;

QY 59 FWDARPPPPAA-----PSFRQVSCLELVARVLQRCERGAKNVLAFGFALLDG----- 106
Db 1084 PRRAAPPCAYLDLEFS-----PSDESESLGGASLGGLPEWFA 1124

QY 107 -----ARGGPEAFTTSVRSYLPNTVTDALRG--SGANGLLRRVGDDVLVHLLARCA 157
Db 1125 DFYPYAEERLGGPPGRYWSV-----DKLGGWRAGSDYLPGRGPP---AWHCRHCA 1172

QY 158 LFVLVAP-----SCAYQVC-----GPPLYQLGNAQARPPPHASGP-----RRRLGCERAWN 204
Db 1173 SLELLPPRHLSCSHDGLDGGWAPP-----PPPWAGPPPPRRRARCGCPRPH 1221

QY 205 HSVREA-GVPLGLPAPGARR--GG-----SASRSL-PLPKRPRRGAAPERT-PVG 252
Db 1222 HRPRASHRAPAAAPHHHRRAAGWDPPFPAPTSSLEDLSSRP-----CP-PHRTGDTG 1276

QY 253 QGSWAHPGRTGPDRCFCVVSP-----ARPAEATSLLEGALSGTRHSHPSVGRQIHA 305
Db 1277 AGTWAHAGALR-----ISPAWSPRYDAAPAPTPTPAAPSVSA---GHGPRGAKWT 1324

QY 306 GPPSTSR-----PPR--PWDTCPP 323
Db 1325 GPSWVGKDRNGFGRTPPGAASCAP 1348
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:19:31 ; Search time 168 Seconds
(without alignments)
2417.152 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPRAPRCRAVRLSLRSHYRE.....TALEAAANPALPSDFKTLTD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_23Sep04:*
- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	2	AAW46957 Human tel
2	5961	100.0	1132	2	AAW90251 Human cat
3	5961	100.0	1132	2	AAV28881 Human tel
4	5961	100.0	1132	2	AAV32090 Human tel
5	5961	100.0	1132	2	AAV43621 A human t
6	5961	100.0	1132	2	AAV26580 Human tel
7	5961	100.0	1132	4	AAV64859 Heart mus
8	5961	100.0	1132	4	AAV64329 Human pro
9	5961	100.0	1132	4	AAV99930 Human tel
10	5961	100.0	1132	4	AAV82765 Human tel
11	5961	100.0	1132	5	AAE29226 Human tel
12	5961	100.0	1132	5	AAU72735 Human tel
13	5961	100.0	1132	6	AAV42384 Human tel
14	5961	100.0	1132	6	AAV42063 Human tel
15	5961	100.0	1132	6	AAV56676 Human tel
16	5961	100.0	1132	6	AAV58045 Human tel
17	5961	100.0	1132	7	ADD21420 Human TER
18	5961	100.0	1132	7	ADH72743 Human pro
19	5961	100.0	1132	8	ADG70114 hTERT pro
20	5961	100.0	1132	8	ADG90599 Human TER
21	5961	100.0	1132	8	ADI82172 Human tel
22	5961	100.0	1154	2	AAW61350 Human tel
23	5961	100.0	1189	2	AAW47008 Glutathio
24	5955	99.9	1285	2	AAW47000 HIS tagge
25	5954	99.9	1132	2	AAW71376 Human tel

26	5954	99.9	1132	2	AAV00627 Human tel
27	5954	99.9	1132	2	AAV00638 Truncated
28	5954	99.9	1132	2	AAV28401 Human EST
29	5954	99.9	1132	3	AAV96566 hEST2, a
30	5954	99.9	1132	7	ADC47061 Human TER
31	5954	99.9	1132	7	ADC40482 Human tel
32	5952	99.8	1132	2	AAW56113 Human tel
33	5927	99.4	1166	2	AAV00647 Telomeras
34	5918	99.3	1405	2	AAW56101 Enhanced
35	5911.5	99.2	1199	2	AAW47007 Glutathio
36	5882	98.7	1120	2	AAV00641 Telomeras
37	5873	98.5	1120	2	AAV00650 Telomeras
38	5721	96.0	1150	2	AAW47006 Glutathio
39	5555	93.2	1053	2	AAV00640 Altered C
40	5516	92.5	1093	2	AAV00649 Altered C
41	5467	91.7	1041	2	AAV00652 Altered C
42	5467	91.7	1041	2	AAV00643 Altered C
43	5008	84.0	948	2	AAV00639 N-termina
44	5004	83.9	948	2	AAV00648 Truncated
45	4932	82.7	936	2	AAV00642 Truncated

ALIGNMENTS

RESULT 1

AAW46957 AAW46957 standard; protein; 1132 AA.

AC AAW46957;

XX XX 73-AUG-1998 (first entry)

XX XX Human telomerase reverse transcriptase.

XX XX Human; telomerase reverse transcriptase; hTERT; TRF; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.

XX XX Homo sapiens.

XX XX 6B2317891-A.

XX XX 08-APR-1998.

XX XX 01-OCT-1997; 97GB-00020890.

XX XX 01-OCT-1996; 96US-00724643.

XX XX 18-APR-1997; 97US-00844419.

XX XX 25-APR-1997; 97US-00846017.

XX XX 06-MAY-1997; 97US-00851843.

XX XX 09-MAY-1997; 97US-00854050.

XX XX 14-AUG-1997; 97US-00911312.

XX XX 14-AUG-1997; 97US-00912951.

XX XX 14-AUG-1997; 97US-00915503.

XX XX (GERO-) GERON CORP.

XX XX (UYTE-) UNIV TECHNOLOGY CORP.

XX XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB; Andrews WH;

XX XX WPI; 1998-171633/16.

XX XX N-PSDB; AAV22379.

XX XX Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.

XX XX Claim 3; Fig 17; 387pp; English.

XX XX The present sequence represents human telomerase reverse transcriptase (hTERT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound

is a modulator of hTERT, by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods

SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQGDPAAPRALVAQCLVCVPW 60
 DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQGDPAAPRALVAQCLVCVPW 60

QY 61 DAPPPAPSPFQVSCLEKELAVQLQRCERGAKNVLAQFALLDARGGPPPAFTSVR 120
 DB 61 DAPPPAPSPFQVSCLEKELAVQLQRCERGAKNVLAQFALLDARGGPPPAFTSVR 120

QY 121 SYLPNTVTDALRSGGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYOVCVGPPLYLQGA 180
 DB 121 SYLPNTVTDALRSGGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYOVCVGPPLYLQGA 180

QY 181 ATQARPPPHASPRRLGCRANVHSVREAGVPLGLPAGARRRGGASRSLPLPKRPRR 240
 DB 181 ATQARPPPHASPRRLGCRANVHSVREAGVPLGLPAGARRRGGASRSLPLPKRPRR 240

QY 241 GAAPERTPVGGWAHPGRTGSDRGFCVUSPARPAEATSLGALSGTHSPSVG 300
 DB 241 GAAPERTPVGGWAHPGRTGSDRGFCVUSPARPAEATSLGALSGTHSPSVG 300

QY 301 ROHAGPPSTSRPRPMDTFCPPVYAEKTHFLYSSGDKQELRPSFLLSLRPSLTGARLL 360
 DB 301 ROHAGPPSTSRPRPMDTFCPPVYAEKTHFLYSSGDKQELRPSFLLSLRPSLTGARLL 360

QY 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLLVOLLRQHSPPWQVYGFVRACLRLVPPGLWGS 480
 DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRLLVOLLRQHSPPWQVYGFVRACLRLVPPGLWGS 480

QY 481 RHNERERLNTKXIFSLGHAKLSLOBLTWKMSVRDCAWLRSPGVCVPAABHRLREI 540
 DB 481 RHNERERLNTKXIFSLGHAKLSLOBLTWKMSVRDCAWLRSPGVCVPAABHRLREI 540

QY 541 LAKFLHLSVYVVELLRFSFYVTTTFOKNRLFFYRKSVWSKLQSIGIRQHLKRVOLRE 600
 DB 541 LAKFLHLSVYVVELLRFSFYVTTTFOKNRLFFYRKSVWSKLQSIGIRQHLKRVOLRE 600

QY 601 LSAEVRQREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRERKAEELTSRVKA 660
 DB 601 LSAEVRQREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRERKAEELTSRVKA 660

QY 661 LFSVLNAYERARRPGLLGASVLGDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
 DB 661 LFSVLNAYERARRPGLLGASVLGDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKFSHVSTLTLDLPQYMRQFVAHL 780

DB 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKFSHVSTLTLDLPQYMRQFVAHL 780
 QY 781 QETSPURDAVLTIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCOGIPQGSILSTL 840
 DB 781 QETSPURDAVLTIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCOGIPQGSILSTL 840
 QY 841 LCLSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
 DB 841 LCLSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
 QY 901 RKTVMNFPVEDBALGTAFAVQMPAHGLFPWCGLLLDRTLLEVSQSDYSSVARTSIRASLTF 960
 DB 901 RKTVMNFPVEDBALGTAFAVQMPAHGLFPWCGLLLDRTLLEVSQSDYSSVARTSIRASLTF 960
 QY 961 NRGFKAGRNRRKLFGLVLRKCHSLFLDLQVNSLQVCTNIYKILLLOAYRHACVQLQP 1020
 DB 961 NRGFKAGRNRRKLFGLVLRKCHSLFLDLQVNSLQVCTNIYKILLLOAYRHACVQLQP 1020

QY 1021 FHQOVWKNPTFFLRVISTDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
 DB 1021 FHQOVWKNPTFFLRVISTDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080

QY 1081 KLTRHRVTYVPLLSGLSRLTAQTOLSRKLPQTTLTALEAAANPALPSDFKTILD 1132
 DB 1081 KLTRHRVTYVPLLSGLSRLTAQTOLSRKLPQTTLTALEAAANPALPSDFKTILD 1132

RESULT 2

AAW90251
 ID AAW90251 standard; protein; 1132 AA.
 XX AC AAW90251;
 XX DT 24-MAY-1999 (first entry)
 XX DE Human catalytic telomerase sub-unit protein.
 XX KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;
 KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
 KW ageing; antisense; neoplastic cell; telomerase-related condition;
 KW tumour cell.
 XX OS Homo sapiens.
 XX PN WO9859040-AZ.
 XX PD 30-DEC-1998.
 XX PF 09-JUN-1998; 98WO-EP003468.
 XX PR 20-JUN-1997; 97DE-01026329.
 PR 26-MAR-1998; 98DE-01013274.
 PR 14-APR-1998; 98DE-01016496.
 XX (FARB) BAYER AG.
 XX PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
 XX WPI; 1999-081276/07.
 DR N-PSDB; AAV72117.
 XX PT New catalytically active subunit of human telomerase - used in the
 PT modulation of telomerase activity, particularly for treating cancer and
 PT ageing.
 XX PS Claim 2; Fig 2; 76pp; German.
 XX CC This sequence represents a novel human catalytic telomerase sub-unit
 CC (hTC). This protein can be used in screening assays to identify
 CC modulators of telomerase and to treat or inhibit cellular disorders,
 CC death, defects and/or other pathological processes involving telomerase,
 CC particularly cancer and ageing (also suitable for this are agents that
 CC stimulate, inhibit or mimic the activity of the subunit). Antisense

CC nucleic acids inhibit telomerase action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed in vivo. Antibodies and fragments of the protein, used as probes or primers, are used to CC diagnose telomerase-related conditions (especially neoplasia) by (i) CC detecting abnormal levels of the subunit protein in body fluids or CC tissues or (ii) by measuring the amount of the encoding nucleic acid. CC Expression of the nucleic acid encoding the subunit mRNA is confined to CC tumour cells, in contrast to the ubiquitous expression of the telomerase CC RNA subunit

XX

Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHREVLPLATFVRRILGPOGWRVLVQRGDPAAPALVAQCLVCVPW 60

DB 1 MPAPRCRAVSLRSHREVLPLATFVRRILGPOGWRVLVQRGDPAAPALVAQCLVCVPW 60

QY 61 DARPPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120

DB 61 DARPPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120

QY 121 SYLPTVTVDALRGSGAMGLLRRVCGDDVLVHLLARCALLFVLVAPSCAYQVCGPPLVOLGA 180

DB 121 SYLPTVTVDALRGSGAMGLLRRVCGDDVLVHLLARCALLFVLVAPSCAYQVCGPPLVOLGA 180

QY 181 ATOARPPPHASGPRRLRCERAWNSVREAGVPLGLPAGARRGGSSASRLPLPKPRR 240

DB 181 ATOARPPPHASGPRRLRCERAWNSVREAGVPLGLPAGARRGGSSASRLPLPKPRR 240

QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPVG 300

DB 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPVG 300

QY 301 ROHAGPSTSRPPRPDTPCPPVYAEKHFILYSGDGKQLRPSFLLSLSPSTGARRL 360

DB 301 ROHAGPSTSRPPRPDTPCPPVYAEKHFILYSGDGKQLRPSFLLSLSPSTGARRL 360

QY 361 VETIFLGRPMPTGTRPLRLPQRYWQMRPLFLELLGNHAOCYGVLLKTHCPRAAVT 420

DB 361 VETIFLGRPMPTGTRPLRLPQRYWQMRPLFLELLGNHAOCYGVLLKTHCPRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQVYGFVACLRRLVPPGLMGS 480

DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQVYGFVACLRRLVPPGLMGS 480

QY 481 RHNERRFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRBEI 540

DB 481 RHNERRFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRBEI 540

QY 541 LAKFLHWMVSVVVELLSRPFYVTTTQKRLFPYKSVMSKLSQSIGIROLKRVQRLRE 600

DB 541 LAKFLHWMVSVVVELLSRPFYVTTTQKRLFPYKSVMSKLSQSIGIROLKRVQRLRE 600

QY 601 LSEAEVROHREARPAALTSRLRFPKPDGLPIVNMDDVVGARTFRREKRAELTSLRKA 660

DB 601 LSEAEVROHREARPAALTSRLRFPKPDGLPIVNMDDVVGARTFRREKRAELTSLRKA 660

QY 661 LFSVLNFERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720

DB 661 LFSVLNFERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTLQPYMQQFVAHL 780

DB 721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTLQPYMQQFVAHL 780

QY 781 QETSPLRDVAIVQSSLINEASSGLFDVFLRPMCHAVIRGKSVQCGIPQGSILSTL 840

DB 781 QETSPLRDVAIVQSSLINEASSGLFDVFLRPMCHAVIRGKSVQCGIPQGSILSTL 840

QY 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVNVL 900

DB 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVNVL 900

QY 901 RKTVVNFVDEALGGTAFVQMPAHGLFPPWCGLLDLTRTLEVSQSDYSYARTSIRASLTF 960

DB 901 RKTVVNFVDEALGGTAFVQMPAHGLFPPWCGLLDLTRTLEVSQSDYSYARTSIRASLTF 960

QY 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIIYKILLQAYRFHACVLQLP 1020

DB 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIIYKILLQAYRFHACVLQLP 1020

QY 1021 FHOQVKNPTFFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL 1080

DB 1021 FHOQVKNPTFFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL 1080

QY 1081 KLTHRRVTVYVPLGLSLRTAQTOLSRKLPGLTTLTALEAAANPALPSDFKTIID 1132

DB 1081 KLTHRRVTVYVPLGLSLRTAQTOLSRKLPGLTTLTALEAAANPALPSDFKTIID 1132

RESULT 3

AAV28881

ID AAV28881 standard; protein; 1132 AA.

AC AAV28881;

XX 17-JAN-2000 (first entry)

XX Human telomerase reverse transcriptase protein.

DE Human telomerase reverse transcriptase protein; hTERT; telomerase; hEST2; catalytic protein component; cell proliferative capacity; DNA primer; telomerase substrate; telomeric DNA synthesis; cell immortality; neoplastic phenotype; diagnostic application; prognostic application; telomerase related condition; cancer; therapeutic agent;

XX telomerase expression; telomerase activity.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Misc-difference 608 /note= "Corresponds to cac codon"

XX

XX WQ950279-A1.

XX 07-OCT-1999.

XX 31-MAR-1999; 99WO-US007160.

XX 31-MAR-1998; 98US-00052919.

XX (GERO-) GERON CORP.

XX (UYTE-) UNIV TECHNOLOGY CORP.

XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB; Andrews WH;

XX WPI; 1999-610834/52.

XX N-PSDB; AAZ08150.

XX Antisense polynucleotides for human telomerase reverse transcriptase used for diagnosing or treating cancer.

XX Claim 2; Fig 2; 31pp; English.

XX The present sequence is human telomerase reverse transcriptase protein. This is the catalytic protein component of telomerase and is also referred to as hEST2. hTERT has the ability to extend a DNA primer that functions as a telomerase substrate for telomeric DNA synthesis. This correlates with cell proliferative capacity, cell immortality, and the development of a neoplastic phenotype. Human hTERT antisense oligonucleotides are useful for diagnostic or prognostic applications to telomerase related conditions, including cancer. They are also useful as

CC	therapeutic agents, for inhibition of telomerase expression and activity
XX	
SQ	Sequence 1132 AA;
	Query Match 100.0%; Score 5961; DB 2; Length 1132;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MPRAPRCRAVRSLSRSHYREVLPLATFVRRILGPGQWRLVQRGDPAAAFRALVAQCLVCVPW 60
Db	1 MPRAPRCRAVRSLSRSHYREVLPLATFVRRILGPGQWRLVQRGDPAAFPALVAQCLVCVPW 60
Qy	61 DARPPPAAPSQRVSCSKELVARVLQRLCERGAKNVLAFGPALLDARGGPPPEAFTTSVR 120
Db	61 DARPPPAAPSQRVSCSKELVARVLQRLCERGAKNVLAFGPALLDARGGPPPEAFTTSVR 120
Qy	121 SYLPTNTVDALRGSGAGLLLRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db	121 SYLPTNTVDALRGSGAGLLLRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Qy	181 ATQARPPPHASGPRRRRLCERAWNHSVREAGVPLGLPAGPARRRGGSASRSLPLPKPRR 240
Db	181 ATQARPPPHASGPRRRRLCERAWNHSVREAGVPLGLPAGPARRRGGSASRSLPLPKPRR 240
Qy	241 GAAPERTPTVQGSWAHPGTRGSDRGFCVVSAPRAEATSLLEGALSGTRSHPSVG 300
Db	241 GAAPERTPTVQGSWAHPGTRGSDRGFCVVSAPRAEATSLLEGALSGTRSHPSVG 300
Qy	301 RQHAGPSTSRPRPMDTPCPPVYAEKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Db	301 RQHAGPSTSRPRPMDTPCPPVYAEKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Qy	361 VETIFLGSRPWMPGTGPRRLPLRPQRYWQMRPLFLELLGNHAQCPVGVLLKTHCPLEAAVT 420
Db	361 VETIFLGSRPWMPGTGPRRLPLRPQRYWQMRPLFLELLGNHAQCPVGVLLKTHCPLEAAVT 420
Qy	421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPWQYGFVRACLRLRVPGLWGS 480
Db	421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPWQYGFVRACLRLRVPGLWGS 480
Qy	481 RHNERFLRNTKKTISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLBEEI 540
Db	481 RHNERFLRNTKKTISLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLBEEI 540
Qy	541 LAKELHWMLSVYVVELLRSFPYVTETTFQKNRLFYKSVWSLQSIGIROHLKRVOLRE 600
Db	541 LAKELHWMLSVYVVELLRSFPYVTETTFQKNRLFYKSVWSLQSIGIROHLKRVOLRE 600
Qy	601 LSEAEVQHREARPALITSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRYKA 660
Db	601 LSEAEVQHREARPALITSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRYKA 660
Qy	661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRQAODPPPELFPVKDVTGAYDTI 720
Db	661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRQAODPPPELFPVKDVTGAYDTI 720
Qy	721 PQDLRTVIAIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPYMQQFVAHL 780
Db	721 PQDLRTVIAIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPYMQQFVAHL 780
Qy	781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRFMCHAVIRGKSVYVQCQIGIPQGSILSTL 840
Db	781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRFMCHAVIRGKSVYVQCQIGIPQGSILSTL 840
Qy	841 LCSLCYGD MENKLPAGIRRDGLLRLVDVDFLLVTPHLTHAKTFLRTLVRGVPYEGCVVNL 900
Db	841 LCSLCYGD MENKLPAGIRRDGLLRLVDVDFLLVTPHLTHAKTFLRTLVRGVPYEGCVVNL 900
Qy	901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTLEEQSDYSYARTSIRASLTFF 960
Db	901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTLEEQSDYSYARTSIRASLTFF 960
Qy	961 NRGFKAGNRMRKLVGLRLKCHSLFDLDQVNSLQTVCTNTYIKTLLQAFHFACVLQLP 1020

Db	961	NRGFKAGNRWRKLFVLRUKCHSLFDLQVNSLQTVCTNIYKLLQLQAYRFHACVQLQ	1020
Qy	1021	FHQQVKNPTFFLRVIRSDTASLCSYILKAKNAGMSLGAKGAGPLPSEAIVQWLCHQAFLL	1080
Db	1021	FHQQVKNPTFFLRVIRSDTASLCSYILKAKNAGMSLGAKGAGPLPSEAIVQWLCHQAFLL	1080
Qy	1081	KLTRHRVTVYVPLLGSLRTAQQLSRKLPGTTLTALFAAANPALPSPDKTILD	1132
Db	1081	KLTRHRVTVYVPLLGSLRTAQQLSRKLPGTTLTALFAAANPALPSPDKTILD	1132
RESULT 4			
AA	Y32090	AA32090 standard; protein; 1132 AA.	
XX	AC	AA32090;	
XX	AC	AA32090;	
DT	XX	17-JAN-2000 (first entry)	
DE	XX	Human telomerase reverse transcriptase (hTERT).	
KW	XX	Telomerase reverse transcriptase; human; hTERT; cell proliferation;	
KW	XX	cancer.	
OS	XX	Homo sapiens.	
PN	XX	WO9950386-A2.	
XX	XX	07-OCT-1999.	
PD	XX	31-MAR-1999; 99WO-US007097.	
PF	XX	31-MAR-1998; 98US-00052864.	
PR	XX	03-AUG-1998; 98US-00128354.	
FA	XX	(GERO-) GERON CORP.	
FI	XX	Morin GB;	
XX	XX	WPI; 1999-610842/52.	
DR	XX	N-PSDB; AA220279.	
PT	XX	New catalytic polypeptide and polynucleotide, useful for increasing	
PT	XX	catalytic activity in a cell.	
PS	XX	Claim 13; Fig 1; 24pp; English.	
CC	XX	The present sequence represents human telomerase reverse transcriptase	
CC	XX	(hTERT). Human telomerase is a target for diagnosing and treating diseases	
CC	XX	relating to cell proliferation and senescence, such as cancer, or for	
CC	XX	increasing the proliferative capacity of a cell. A claimed method for	
CC	XX	increasing the proliferative capacity of a vertebrate cell, especially a	
CC	XX	human or other mammalian cell, involves introducing into the cell a	
CC	XX	recombinant hTERT polynucleotide encoding an hTERT variant in which	
CC	XX	residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323	
CC	XX	and 415-450, or 192-271 and 415-450 of the present sequence are deleted.	
CC	XX	A claimed method of preparing recombinant telomerase involves contacting	
CC	XX	a recombinant hTERT deletion mutant (as above) with a telomerase RNA	
CC	XX	component such that the 2 proteins associate to form a complex capable of	
CC	XX	catalysing the addition of nucleotides to a telomerase substrate. A	
CC	XX	claimed method for reducing telomerase activity in a cell involves	
CC	XX	introducing a recombinant polynucleotide encoding an hTERT variant having	
CC	XX	a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or	
CC	XX	1055-1071 of the present sequence	
SQ	XX	Sequence 1132 AA;	
Query Match			
Best Local Similarity 100.0%; Score 5961; DB 2; Length 1132;			
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MPRAPRCRAVRSLLRSHRYEVLPLATFVRLRGQGWRLVQRGDPAAFRALVAQCLVCVPW	60

Db 1 MPRAPRCRAVSLRSHYREVLPLATFVRRLPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
Db 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
QY 121 SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGSSRSRLPLPKPRR 240
Db 181 ATOARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGSSRSRLPLPKPRR 240
QY 241 GAAPEPERTPVQGSWAHPGTRGPSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPEPERTPVQGSWAHPGTRGPSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
QY 301 RQHAGPPSTSRPRPMDTPCPVYAEKHFLLYSGGDKQLRPSFLJSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPRPMDTPCPVYAEKHFLLYSGGDKQLRPSFLJSSLRPSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCYPGVLLKTHCPFLRAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCYPGVLLKTHCPFLRAVT 420
QY 421 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRHSSPWQVYFVRACLRLRLVPPGLWGS 480
Db 421 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRHSSPWQVYFVRACLRLRLVPPGLWGS 480
QY 481 RHNERFLRNTKXIFSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVCPVPAEHLREEI 540
Db 481 RHNERFLRNTKXIFSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVCPVPAEHLREEI 540
QY 541 LAKFLHMLMSVYVELLRSPFYVTETTPQKNRLFYRKSVWSKLQSGIROLKRVQURE 600
Db 541 LAKFLHMLMSVYVELLRSPFYVTETTPQKNRLFYRKSVWSKLQSGIROLKRVQURE 600
QY 601 LSEAEVQHRARPALLTSRLRF1PKDGLRPIVNMDDVVCARTFREKRAERTLSRKA 660
Db 601 LSEAEVQHRARPALLTSRLRF1PKDGLRPIVNMDDVVCARTFREKRAERTLSRKA 660
QY 661 LFSVLNERARRPGLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNERARRPGLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVVOCQIPGSGIISLTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVVOCQIPGSGIISLTL 840
QY 841 LCSLYGDMENKLFAGIRRDGILLRLVDDFLVLTPLTHAKTFLRTLVRGPEYGCVVNL 900
Db 841 LCSLYGDMENKLFAGIRRDGILLRLVDDFLVLTPLTHAKTFLRTLVRGPEYGCVVNL 900
QY 901 RKTVVNFPVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQDSSYARTSIRASLTF 960
Db 901 RKTVVNFPVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQDSSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLPGLVRLKCHSLFDLQVNSIQVCTNLYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNRMRKLPGLVRLKCHSLFDLQVNSIQVCTNLYKILLQAYRFHACVLQLP 1020
QY 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTRHRTVYVPLLGSLRTAQQLSRKLPFGTTLTALAAANPALSPDFKTLTD 1132

Db 1081 KLTRHRTVYVPLLGSLRTAQQLSRKLPFGTTLTALAAANPALSPDFKTLTD 1132
RESULT 5
AY43621
ID AAY43621 standard; protein; 1132 AA.
XX AC AAY43621;
XX DT 26-JAN-2000 (first entry)
XX DE A human telomerase reverse transcriptase (TRT) polypeptide.
XX KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
XX KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
XX KW immunological destruction; telomerase; cancer; proliferation disease.
XX OS Homo sapiens.
XX PN WO9950392-A1.
XX PD 07-OCT-1999.
XX PF 30-MAR-1999; 99WO-US0006898.
XX PR 31-MAR-1998; 98US-0112006P.
XX PA (GERO-) GERON CORP.
XX PI Gaeta FCA;
XX DR WPI; 1999-610845/52.
XX DR N-PSDB; AAZ30154.
XX PT Eliciting an in vivo immune response for prevention and treatment of
XX PT cancers.
XX PS Claim 3; Fig 1; 26pp; English.
XX CC The present sequence represents a human telomerase reverse transcriptase
XX CC (TRT) polypeptide. The protein is used in the method of the invention.
XX CC The specification describes a method for activating a T lymphocyte,
XX CC comprising contacting the T lymphocyte with a dendritic cell that
XX CC expresses a TRT peptide in the context of a MHC class I or MHC class II
XX CC molecule. The protein causes induction of an in vivo immunological
XX CC response to telomerase activity. Cancer cells are characterized by
XX CC expression of endogenous TRT gene and the presence of detectable
XX CC telomerase activity. Therefore, by eliciting a specific immune response
XX CC to TRT or to TRT-expressing cells, it is possible to selectively target
XX CC proliferating cells for immunological destruction. The method is used for
XX CC eliciting an in vivo immune response to telomerase by activating a T
XX CC lymphocyte, and is useful for prevention and treatment of cancers and
XX CC other proliferation diseases/conditions
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVSLRSHYREVLPLATFVRRLPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVSLRSHYREVLPLATFVRRLPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
Db 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
QY 121 SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGSSRSRLPLPKPRR 240

Db 181 ATQARPPHAGPRRRIGCCRAMHNSVREAGVPLGLPAPGARRGGSASRLPLPKRRP 240
Qy 241 GAAPEPERTVQGGSWAHPGRTGSDRGFCVWSPAPAEATSLGALSCTGTHSHPSVG 300
Db 241 GAAPEPERTVQGGSWAHPGRTGSDRGFCVWSPAPAEATSLGALSCTGTHSHPSVG 300
Qy 301 RQHAGPPSTSRPPRPWDTPCPVYAEKHFVYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPRPWDTPCPVYAEKHFVYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLRQHSPPWQVYFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLRQHSPPWQVYFVRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKXIFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKXIFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKFLHLMVSVYVELLSRFYVTETTFQKNRLFYRKSVWSKLQSIGIRQHLKRVQVRE 600
Db 541 LAKFLHLMVSVYVELLSRFYVTETTFQKNRLFYRKSVWSKLQSIGIRQHLKRVQVRE 600
Qy 601 LSAEVRQREARPAALLTSRLRTPKPDGLRPIVNDYVVGATFERREKRAELTSRVKA 660
Db 601 LSAEVRQREARPAALLTSRLRTPKPDGLRPIVNDYVVGATFERREKRAELTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDADVIVQSSSLNEASGLFDVFLRFCHHAVIRGKSYVQCQIPGGSILSTL 840
Db 781 QETSPLRDADVIVQSSSLNEASGLFDVFLRFCHHAVIRGKSYVQCQIPGGSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDELLVTPHLTHAKTEFLRLTVRGVPEYGCVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDELLVTPHLTHAKTEFLRLTVRGVPEYGCVNL 900
Qy 901 RKTVMFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYVARTSIRASLTF 960
Db 901 RKTVMFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYVARTSIRASLTF 960
Qy 961 NRGFKAGRNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGRNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
Qy 1021 FHQVQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQVQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTVYVPLGLSRLTAQTQLSRKLPGTTLTALAEAAANPALPSPDKTILD 1132
Db 1081 KLTRHRVTVYVPLGLSRLTAQTQLSRKLPGTTLTALAEAAANPALPSPDKTILD 1132

RESULT 6
AA26580
ID AAY26580 standard; protein; 1132 AA.
XX
AC AAY26580;
XX
DT 13-SEP-1999 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT) enzyme.

XX
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay; immunogen; enzyme; telomerase-mediated DNA replication; human.
OS Homo sapiens.
XX
FN WO9927113-AL.
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US025211.
XX
PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX
(GERO-) GERON CORP.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX
PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and nucleic acids.
XX
PS Disclosure; Fig 3; 135pp; English.
XX
CC The invention relates to a mouse telomerase reverse transcriptase (mTERT) enzyme. Compositions containing mTERT can be used in telomere length assays. Isolated mTERT is useful as an immunogen for the production of monoclonal or polyclonal antibodies. The method is useful for assessing the degree of purification and identification of new mTERT species, such as an mTERT allele, homolog or isoform, or to screen for modulators (antagonists and agonists) of telomerase-mediated DNA replication. CC Antagonists and agonists of mTERT can be used to modify the activity of other telomerase enzymes such as human TERT (hTERT). The present sequence CC represents a human TERT enzyme
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPAAPSPFQVSCLEKELVARVQLRCLERCAGKNVLAFGFALLDGARGGPEAFTTSVR 120
Db 61 DARPPAAPSPFQVSCLEKELVARVQLRCLERCAGKNVLAFGFALLDGARGGPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGANGLLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
Db 121 SYLPNTVTDALRGSGANGLLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
Qy 181 ATQARPPPHASGPRRLGGERAWNSHVRAGVPLGLPAPGARRGGSASRLPLPKRRP 240
Db 181 ATQARPPPHASGPRRLGGERAWNSHVRAGVPLGLPAPGARRGGSASRLPLPKRRP 240
Qy 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVWSPAPAEATSLGALSCTGTHSHPSVG 300
Db 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVWSPAPAEATSLGALSCTGTHSHPSVG 300
Qy 301 ROHAGPPSTSRPPRPWDTPCPVYAEKHFVYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPPSTSRPPRPWDTPCPVYAEKHFVYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLRQHSPPWQVYFVRACLRRLVPPGLWGS 480

Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGVFRACLRRLRVPGLWGS 480
Qy 481 RHNERRFLRNTKKFISLGKHAHKLISLOELTWKMSVRDCAWLRSSPGVGVCPAAEHLREEI 540
Db 481 RHNERRFLRNTKKFISLGKHAHKLISLOELTWKMSVRDCAWLRSSPGVGVCPAAEHLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFVTTTQKNRFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFVTTTQKNRFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600
Qy 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELVFKVDVGTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELVFKVDVGTGAYDTI 720
Qy 721 QDRLTEVIAIIKPNQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 721 QDRLTEVIAIIKPNQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Qy 781 QETSPDRADVIEOSSSNEASSGLFDVFLRPMCHHVRIRCKSVYQCGIPQGSILSTL 840
Db 781 QETSPDRADVIEOSSSNEASSGLFDVFLRPMCHHVRIRCKSVYQCGIPQGSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFURTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFURTLVRGVPEYGCVVNL 900
Qy 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDRTTLEVSQSDYSYARTSIRASLTF 960
Db 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDRTTLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
Db 961 NRGFKAGNMRRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
Qy 1021 FHOQVKNPFFLVIISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWMLCHOAFL 1080
Db 1021 FHOQVKNPFFLVIISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWMLCHOAFL 1080
Qy 1081 KLTRHRTVYVPLLSGLRTAQQLSRKLPFGTTLTALEAAANPALPSDFKTLID 1132
Db 1081 KLTRHRTVYVPLLSGLRTAQQLSRKLPFGTTLTALEAAANPALPSDFKTLID 1132

RESULT 7

AAG64859
ID AAG64859 standard; protein; 1132 AA.
AC AAG64859;
XX
DT 21-SEP-2001 (first entry)
DE Heart muscle cell differentiation related protein SEQ ID NO: 31.
XX
KW Heart muscle cell; human; cell differentiation; heart disease.
XX
OS Homo sapiens.
XX
PN W0200148151-A1.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-JP009323.
XX
PR 28-DEC-1999; 99JP-00372826.
PR 28-FEB-2000; 2000WO-JP001148.
PR 02-NOV-2000; 2000WO-JP007741.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.

XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI Yamada Y;
XX
DR WPI; 2001-425656/45.
DR N-PSDB; AAH48235.
XX
PT Cells capable of differentiating into cardiomyocytes and originating in
PT bone marrow or umbilical blood cells for study of cardiomyocyte
PT differentiation and treatment of heart disease.
XX
PS Claim 87; Page 143-147; 183pp; Japanese.
XX
CC The present invention provides cells originating in the human bone marrow
CC or umbilical blood cells which are capable of differentiating into
CC cardiomyocytes. These cells are useful in the treatment of diseases
CC involving heart muscle degeneration, such as myocardial infarction, and
CC the study of cardiomyocyte differentiation. The present sequence is a
CC protein described in the exemplification of the invention
XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVORGDPAAFRALVAOCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVORGDPAAFRALVAOCLVCVPW 60
Qy 61 DARPPPAAPFRQVSCLELVARVQLRCERGAKNVLAFAFGALLDARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPFRQVSCLELVARVQLRCERGAKNVLAFAFGALLDARGGPPPEAFTTSVR 120
Qy 121 SYLNTVTDALRSGGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQCGPPLYQLGA 180
Db 121 SYLNTVTDALRSGGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGCARRRGGASRLPLPKPRR 240
Db 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGCARRRGGASRLPLPKPRR 240
Qy 241 GAAPEPERTVPGQSWAHPGRTGSPDRGFCVVSAPARPAEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPERTVPGQSWAHPGRTGSPDRGFCVVSAPARPAEATSLEGALSGTRHSHPSVG 300
Qy 301 RQHAGPPSTSRPRPMDTPCPVYATKHFLLSSGDKQELRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPRPMDTPCPVYATKHFLLSSGDKQELRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMPPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMPPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGVFRACLRRLRVPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGVFRACLRRLRVPGLWGS 480
Qy 481 RHNERRFLRNTKKFISLGKHAHKLISLOELTWKMSVRDCAWLRSSPGVGVCPAAEHLREEI 540
Db 481 RHNERRFLRNTKKFISLGKHAHKLISLOELTWKMSVRDCAWLRSSPGVGVCPAAEHLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFVTTTQKNRFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFVTTTQKNRFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600
Qy 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELVFKVDVGTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELVFKVDVGTGAYDTI 720

QY 721 PODRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
QY 781 QETSPLRDAVTEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVQCQGIPOQSILSTL 840
DB 781 QETSPLRDAVTEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVQCQGIPOQSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHPLTHAKTFLRTLVRGVPEYGCVVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHPLTHAKTFLRTLVRGVPEYGCVVNL 900
QY 901 RKTVVNFVEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTIF 960
DB 901 RKTVVNFVEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTIF 960
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
DB 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
QY 1021 FHOQWKNPTEFLRIVISDTASLCYSILKAKVAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHOQWKNPTEFLRIVISDTASLCYSILKAKVAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTRHRVTVYVPLLSGLRTAQQLSRKLP GTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTVYVPLLSGLRTAQQLSRKLP GTTLTALEAAANPALPSDFKTILD 1132

RESULT 8

AAG64329

ID AAG64329 standard; protein; 1132 AA.

XX AC AAG64329;

XX DT 24-SEP-2001 (first entry)

XX XX Human protein #2.

XX KW Angiogenesis; cardiatic; cell differentiating agent; bone marrow;

XX KW heart muscle cell; heart disease; human.

XX OS Homo sapiens.

XX XX WO200148149-A1.

XX XX 05-JUL-2001.

XX XX 28-FEB-2000; 2000WO-JP001148.

XX XX 28-DEC-1999; 99JP-00372826.

XX XX (KYOW) KYOWA HAKKO KOGYO KK.

XX XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;

XX XX WPI; 2001-418252/44.

XX XX N-PSDB; AAH49601.

XX XX New adult bone marrow-originated cells capable of differentiating into

XX XX heart muscle cells, applicable as remedies for various heart diseases

XX XX particularly with damaged heart muscle accompanying degeneration.

XX XX Disclosure; Page 128-134; 158pp; Japanese.

XX XX The present invention relates to cells isolated from bone marrow, which

XX XX are capable of at least differentiating into heart muscle cells. The

XX XX cells are applicable as remedies for various heart diseases particularly

XX XX with damaged heart muscle accompanying degeneration. The present sequence

XX XX was used to illustrate the present invention

XX XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPPCRAVRSLLRSHYREVLPATFVRLPGQGRHLVQRGDPAPAFRALVAOCLVCVPW 60
DB 1 MPAPPCRAVRSLLRSHYREVLPATFVRLPGQGRHLVQRGDPAPAFRALVAOCLVCVPW 60
QY 61 DARPPPAASFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGCARGGPPPEAFTTSVR 120
DB 61 DARPPPAASFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGCARGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLVHLLARCALEFVLVAPSCAYQVCGPPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLVHLLARCALEFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATOAREPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSPLPKRPRR 240
DB 181 ATOAREPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSPLPKRPRR 240
QY 241 GAAPEPERTPVQGGSWAHPGRTGRGSDRGFCVVSAPPAEATSLGALSGRTRHSHPSVG 300
DB 241 GAAPEPERTPVQGGSWAHPGRTGRGSDRGFCVVSAPPAEATSLGALSGRTRHSHPSVG 300
QY 301 ROHAGPPSTSRPPRPWDTPCPVVAETHKFLYSSGDKEQLRPSFLLSLRPSLTGARL 360
DB 301 ROHAGPPSTSRPPRPWDTPCPVVAETHKFLYSSGDKEQLRPSFLLSLRPSLTGARL 360
QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFELGLGNHACQPYGVLLKTHCPRAAVT 420
DB 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFELGLGNHACQPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPOGSVAAPPEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRLRVLPPGLWGS 480
DB 421 PAAGVCAREKPOGSVAAPPEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRLRVLPPGLWGS 480
QY 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAEHLRBEI 540
DB 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAEHLRBEI 540
QY 541 LAKFLHLMWSVYVVELLSRFFVVTETTFQKRLFPYRKSVMSKLSQISIGIROHLKRVQRE 600
DB 541 LAKFLHLMWSVYVVELLSRFFVVTETTFQKRLFPYRKSVMSKLSQISIGIROHLKRVQRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNAYERARRPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNAYERARRPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
DB 721 PQDLRLTEVIASIIKQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
QY 781 QETSPLRDAVTEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVQCQGIPOQSILSTL 840
DB 781 QETSPLRDAVTEIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVQCQGIPOQSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHPLTHAKTFLRTLVRGVPEYGCVVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHPLTHAKTFLRTLVRGVPEYGCVVNL 900
QY 901 RKTVVNFVEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTIF 960
DB 901 RKTVVNFVEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTIF 960
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
DB 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020

Qy 1021 FHOQWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAFLL 1080
Db 1021 FHOQWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVLLGSLRTAQQLSRKLPQTTLTLEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVLLGSLRTAQQLSRKLPQTTLTLEAAANPALPSDFKTILD 1132

RESULT 9

AAB99930
ID AAB99930 standard; protein; 1132 AA.
XX AAB99930;
AC AAB99930;
XX
DT 26-SEP-2001 (first entry)
XX Human telomerase protein sequence SEQ ID NO:31.

DE
XX Differentiation; heart muscle cell; cytokine; transcription factor;
KW proliferation; surface antigen; heart disease; cardiomyocyte;
KW bone marrow; umbilical blood cell; heart muscle degeneration;
KW myocardial infarction.

XX Homo sapiens.
OS
XX WO200148150-A1.
XX
XX 05-JUL-2001.

XX 02-NOV-2000; 2000WO-JP007741.

XX 28-DEC-1999; 99JP-00372826.

XX 28-FEB-2000; 2000WO-JP001148.

XX (KYO) KYOWA HAKKO KOGYO KK.

XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;

PI Yamada Y;

XX WPI; 2001-425655/45.

DR N-FSDB; AAH44366.

XX Cells capable of differentiating into cardiomyocytes and originating in
PT bone marrow or umbilical blood cells for study of cardiomyocyte
PT differentiation and treatment of heart disease.

XX Claim 146; Page 137-141; 187pp; Japanese.

XX The present invention describes cells originating in bone marrow or
CC umbilical blood cells which are capable of differentiating into
CC cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
CC differentiation of the cells; (2) a method for carrying out the
CC differentiation into cardiomyocytes, regulated by a promotional and/or
CC inhibitory factor; (3) a method for the differentiation of the cells into
CC cell types other than cardiomyocytes; (4) drug compositions promoting the
CC formation of heart muscle and regeneration of heart tissue which contain
CC the cells; (5) a method for the production of antibodies which recognise
CC the cells, especially antibodies which recognise a surface antigen on the
CC cells; (6) a method for screening factors which promote the proliferation
CC of the cells; (7) a method for immortalising the cells by expressing
CC telomerase in them; (8) drug compositions for the treatment of heart
CC disease which contain the immortalised cells; and (9) cell-free
CC supernatant from the culture of the cells and its use in promoting their
CC differentiation into cardiomyocytes. The cells are used in the treatment
CC of diseases involving heart muscle degeneration, such as myocardial
CC infarction and in the study of cardiomyocyte differentiation. AAH44351 to
CC AAH44409 and AAB99915 to AAB99935 represent sequences used in the
CC exemplification of the present invention

XX Sequence 1132 AA;

SQ Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWELVQRGDPAAPRALVAOQLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWELVQRGDPAAPRALVAOQLVCVPW 60
Qy 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDARGGPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Qy 181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPKPARR 240
Db 181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPKPARR 240
Qy 241 GAAPEPERTVPGQGSWAHPQRTGRPSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPERTVPGQGSWAHPQRTGRPSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300
Qy 301 ROHHAGPPSTSRPPRWDTPCPVYAEKHFLYSSGDKQLRPSFLSLRPSLTGARRL 360
Db 301 ROHHAGPPSTSRPPRWDTPCPVYAEKHFLYSSGDKQLRPSFLSLRPSLTGARRL 360
Qy 361 VETIFLGSRPWMPGTPRRLPRLPORVWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTPRRLPRLPORVWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRELVLQRLRHSSFPWQYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSAVAPEEEDTPRELVLQRLRHSSFPWQYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERFLRNTKFIISLGKHAKLQBELTWKMSVRDCAWLRSPSGVGCVPAAEHLREBI 540
Db 481 RHNERFLRNTKFIISLGKHAKLQBELTWKMSVRDCAWLRSPSGVGCVPAAEHLREBI 540
Qy 541 LAKFLHMLMSVYVVELLRSFFYTETTFQKNRFFYRKSVMKLSQSIGIRHLKRVOLRE 600
Db 541 LAKFLHMLMSVYVVELLRSFFYTETTFQKNRFFYRKSVMKLSQSIGIRHLKRVOLRE 600
Qy 601 LSEAEVQRHREARPALITSRLRFTPKDGLRPIVNM DYVVGARTFREKRAERLTSRKA 660
Db 601 LSEAEVQRHREARPALITSRLRFTPKDGLRPIVNM DYVVGARTFREKRAERLTSRKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 POBELTEVIASIIKPQNTYCVRRYAVYQKAAHGHVRKAFKSHVSTLTLQPYMFOFAHL 780
Db 721 POBELTEVIASIIKPQNTYCVRRYAVYQKAAHGHVRKAFKSHVSTLTLQPYMFOFAHL 780
Qy 781 QETSPLRDADVIVQSSSLNEASGLFDVFLRFMCHHAVIRGKSYVOCQIGIPOGSIISLT 840
Db 781 QETSPLRDADVIVQSSSLNEASGLFDVFLRFMCHHAVIRGKSYVOCQIGIPOGSIISLT 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLLVTPH LTHAKTFLRTILVRGVEPYGCVVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLLVTPH LTHAKTFLRTILVRGVEPYGCVVNL 900
Qy 901 RKTVMNPFVDEALGGTAFVOMPAHGLFPWCGLLDTRTLEQSDYSYARTSIRASLTFF 960
Db 901 RKTVMNPFVDEALGGTAFVOMPAHGLFPWCGLLDTRTLEQSDYSYARTSIRASLTFF 960
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Db 961 NRGFKAGNNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Qy 1021 FHOQWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAFLL 1080

Db 1021 FHQOVKNPTFFLRVIRSDTASLCVSLKAKNAGKMSLGAKGAAGLPSEAVQWICHOAFLL 1080
QY 1081 KLTRHRYVYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSPDKTILD 1132
|||||
Db 1081 KLTRHRYVYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSPDKTILD 1132
|||
RESULT 10
AAB82765
ID AAB82765 standard; protein; 1132 AA.
XX
AC AAB82765;
XX
XX 29-OCT-2001 (first entry)
XX Human telomerase reverse transcriptase.
XX
XX Telomerase reverse transcriptase; hTERT; human; cancer; tumour;
KW cytotoxic T lymphocyte; major histocompatibility complex;
KW human leucocyte antigen; HLA-A2.1; vaccine.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 13..21
FT /note= "HLA-A2.1 binding motif"
FT Peptide 23..31
FT /note= "HLA-A2.1 binding motif"
FT Peptide 76..84
FT /note= "HLA-A2.1 binding motif"
FT Peptide 96..104
FT /note= "HLA-A2.1 binding motif"
FT Peptide 140..148
FT /note= "HLA-A2.1 binding motif"
FT Peptide 152..160
FT /note= "HLA-A2.1 binding motif"
FT Peptide 346..354
FT /note= "HLA-A2.1 binding motif"
FT Peptide 353..361
FT /note= "HLA-A2.1 binding motif"
FT Peptide 371..379
FT /note= "HLA-A2.1 binding motif"
FT Peptide 388..396
FT /note= "HLA-A2.1 binding motif"
FT Peptide 407..415
FT /note= "HLA-A2.1 binding motif"
FT Peptide 487..495
FT /note= "HLA-A2.1 binding motif"
FT Peptide 540..548
FT /label= p540
FT /note= "HLA-A2.1 binding motif"
FT Peptide 548..556
FT /note= "HLA-A2.1 binding motif"
FT Peptide 555..563
FT /note= "HLA-A2.1 binding motif"
FT Peptide 572..580
FT /note= "HLA-A2.1 binding motif"
FT Peptide 705..713
FT /note= "HLA-A2.1 binding motif"
FT Peptide 724..732
FT /note= "HLA-A2.1 binding motif"
FT Peptide 772..780
FT /note= "HLA-A2.1 binding motif"
FT Peptide 797..805
FT /note= "HLA-A2.1 binding motif"
FT Peptide 812..820
FT /note= "HLA-A2.1 binding motif"
FT Peptide 836..844
FT /note= "HLA-A2.1 binding motif"
FT Peptide 863..871
FT /note= "HLA-A2.1 binding motif"
FT Peptide 865..873
FT /label= p865

FT Peptide /note= "HLA-A2.1 binding motif"
FT 883..891
FT /note= "HLA-A2.1 binding motif"
FT Peptide 926..934
FT /note= "HLA-A2.1 binding motif"
FT Peptide 934..942
FT /note= "HLA-A2.1 binding motif"
FT Peptide 969..977
FT /note= "HLA-A2.1 binding motif"
FT Peptide 988..996
FT /note= "HLA-A2.1 binding motif"
FT Peptide 1072..1080
FT /note= "HLA-A2.1 binding motif"
FT Peptide 1079..1087
FT /note= "HLA-A2.1 binding motif"
FT Peptide 1095..1103
FT /note= "HLA-A2.1 binding motif"
FT Peptide 1122..1130
FT /note= "HLA-A2.1 binding motif"
XX
XX WO200160391-A1.
XX
XX 23-AUG-2001.
XX
XX 15-FEB-2001; 2001WO-US005143.
XX
XX 15-FEB-2000; 2000US-0182685P.
PR 15-FEB-2001; 2001US-00182685.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Zanetti M;
PI
XX WPI; 2001-536552/59.
DR
XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
FT for treating cancers or tumors or for inducing immune response against
FT tumors, comprises a telomerase reverse transcriptase peptide.
XX
PS Disclosure; Fig 5; 52pp; English.
XX
XX The present sequence is that of human telomerase reverse transcriptase
CC (hTERT). The sequence was analysed for 9-mer peptide sequences containing
CC known binding motifs for the human leukocyte antigen HLA-A2.1 molecule.
CC From an initial panel of about 30 candidate peptides, 2 sequences,
CC denoted p540 (see AAB82772) and p865 (see AAB82773), were examined. The
CC majority of healthy individuals as well as patients with prostate cancer
CC immunised in vitro against these 2 HLA-A2.1 restricted peptides developed
CC hTERT-specific cytotoxic T lymphocytes (CTL). The cancer patients' CTL
CC specifically lysed a variety of HLA-A2+ cancer cell lines such as
CC prostate, breast, colon, lung and melanoma, demonstrating immunological
CC recognition of endogenously-processed hTERT peptides. In vivo immunisation
CC of HLA-A2.1 transgenic mice generated a specific CTL response against
CC both hTERT peptides. The induction of CTL responses in vitro and in vivo,
CC and the susceptibility to lysis of tumour cells of various origins by
CC hTERT CTL suggest that hTERT could serve as a universal cancer vaccine for
CC humans. Thus, a claimed universal vaccine for treating tumours of any
CC origin comprises at least 1 hTERT peptide in an amount effective for
CC initiating and enhancing a CTL response against cancer cells. The peptide
CC is 7-15 amino acid residues in length and may be modified to enhance
CC binding to the major histocompatibility complex. Also claimed is a method
CC for inducing and enhancing a CTL response against cancer cells, involving
CC harvesting blood leucocytes, pulsing with hTERT, and contacting cancer
CC cells with the pulsed leucocytes. A method for targeting CTL to tumour
CC cells is also claimed, and involves administering a hTERT peptide to a
CC mammal, especially a cancer patient
XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRVRSLLRSHYREVLPATFVRRRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60
DB 1 MPRAPCRVRSLLRSHYREVLPATFVRRRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
DB 61 DARPPPAAPSFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
QY 121 SYLNTVTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRRRLCERANWHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240
DB 181 ATQARPPPHASGPRRRRLCERANWHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300
DB 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300
QY 301 RQHHAGPSTSRPRPMDTPCPPVYAEKHFYSSGDKQELRPSFLSSLRPSLTGARRL 360
DB 301 RQHHAGPSTSRPRPMDTPCPPVYAEKHFYSSGDKQELRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGRPMWGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPMWGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKQGSVAAPAEEDTDPRLVQLLRHSSPWQYVFRACLRLRVPGLWGS 480
DB 421 PAAGVCAREKQGSVAAPAEEDTDPRLVQLLRHSSPWQYVFRACLRLRVPGLWGS 480
QY 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI 540
DB 481 RHNERRFLRNTKKFISLGKHAQLSLOELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLHLMMSYVVVELLRSPFYVTETTFQKNRPFYRKSVMSKLSQSIGIROLKRVQLRE 600
DB 541 LAKFLHLMMSYVVVELLRSPFYVTETTFQKNRPFYRKSVMSKLSQSIGIROLKRVQLRE 600
QY 601 LSEAEVQRHRAARALLTSRLRFIPKPDGLRPIVNDYVVCARTFREKRAERLTSRVKA 660
DB 601 LSEAEVQRHRAARALLTSRLRFIPKPDGLRPIVNDYVVCARTFREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLGASVLGDDIHRAWTFVLVRAPDPPPELVKVDVGTGAYDTI 720
DB 661 LFSVLNTERARRPGLGASVLGDDIHRAWTFVLVRAPDPPPELVKVDVGTGAYDTI 720
QY 721 PODRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDVAVIEOSSSLNEASSGLFDVFLRPMCHHAVIRGKSYVOCQGIPOQSII STL 840
DB 781 QETSPLRDVAVIEOSSSLNEASSGLFDVFLRPMCHHAVIRGKSYVOCQGIPOQSII STL 840
QY 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVLTPLTHAKTELRTLVRGVPEYGCVVNL 900
DB 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVLTPLTHAKTELRTLVRGVPEYGCVVNL 900
QY 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQDYSYARTSIRASITF 960
DB 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQDYSYARTSIRASITF 960
QY 961 NRGFKAGRMKRLFGVULRLKCHSLFLDLQVNSIQTVCTNIYKILLQAVRFHACVLOLP 1020
DB 961 NRGFKAGRMKRLFGVULRLKCHSLFLDLQVNSIQTVCTNIYKILLQAVRFHACVLOLP 1020
QY 1021 FHOQVKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHOQVKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTRHRVTYVPLLGSRLTAQQLSRKLP GTTTLTALEAAANPALPSDFKTILD 1132

DB 1081 KLTRHRVTYVPLLGSRLTAQQLSRKLP GTTTLTALEAAANPALPSDFKTILD 1132
RESULT 11
AAE29226
ID AAE29226 standard; protein; 1132 AA.
XX AAE29226;
XX AC
XX 27-JAN-2003 (first entry)
XX Human telomerase reverse transcriptase (TERT).
XX Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
XX transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
XX telomerase reverse transcriptase.
XX Homo sapiens.
XX OS
XX WO200274948-A2.
XX FN
XX 26-SEP-2002.
XX PD
XX 21-MAR-2002; 2002WO-CA000378.
XX PF
XX 21-MAR-2001; 2001US-0277811P.
XX PR
XX (GERO-) GERON CORP.
XX PA
XX Denning C, Clark AJ, Schiff JM;
XX PI
XX WPI: 2002-759895/82.
XX DR N-PSDB; AAD46821.
XX DR
XX Mammalian cells, useful for producing animal tissues with carbohydrate
XX PT antigens that are compatible for transplantation into human patients.
XX PS
XX Disclosure; Page 34; 71pp; English.
XX XX
CC The invention relates to animal tissues with carbohydrate antigens that
CC are compatible for transplantation into human patients. The mammalian
CC cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC with carbohydrate antigens that are compatible for transplantation into
CC human patients. The present sequence is human telomerase reverse
CC transcriptase (TERT) used in the invention
XX SQ
Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 5; Length 1132;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPCRVRSLLRSHYREVLPATFVRRRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60
DB 1 MPRAPCRVRSLLRSHYREVLPATFVRRRLPGQWRLVORGDDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
DB 61 DARPPPAAPSFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEAFTTSVR 120
QY 121 SYLNTVTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRRRLCERANWHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240
DB 181 ATQARPPPHASGPRRRRLCERANWHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300
DB 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVG 300

Db 361 VETIFLGRSRPMPGTPRRLLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPFLRAAVT 420
Qy 421 PAAGVCAREKPGQSSVAAPPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSSVAAPPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFIISLGKHAHKLQELTWKMSVDRCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKFIISLGKHAHKLQELTWKMSVDRCAWLRRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKELHMLMSVYVVELLRSFYVTETTFQKNRLEFFYKSVMSKLSQIGIROHLKRVOLRE 600
Db 541 LAKELHMLMSVYVVELLRSFYVTETTFQKNRLEFFYKSVMSKLSQIGIROHLKRVOLRE 600
Qy 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSRVKA 660
Db 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKKAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 QDRLTEVIASIIKPQNTYCYRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 QDRLTEVIASIIKPQNTYCYRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLDADVIEOSSLSNEASSGLFDVFLRFPMCHHVRIRGKSVVQCOGIPQGSILSTL 840
Db 781 QETSPLDADVIEOSSLSNEASSGLFDVFLRFPMCHHVRIRGKSVVQCOGIPQGSILSTL 840
Qy 841 LCSICYGDMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSICYGDMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
Qy 901 RKTVNVPEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVDQSDYSYARTSIRASLTIF 960
Db 901 RKTVNVPEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVDQSDYSYARTSIRASLTIF 960
Qy 961 NRGFKAGNMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Db 961 NRGFKAGNMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Qy 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRRVTYVPLLGSLRTAQTLQRKLPQTTLTALAAAANPALPSPDKTILD 1132
Db 1081 KLTHRRVTYVPLLGSLRTAQTLQRKLPQTTLTALAAAANPALPSPDKTILD 1132

RESULT 13

ABR42384
ID ABR42384 standard; protein; 1132 AA.

AC ABR42384;

XX ABR42384;

DT 11-AUG-2003 (first entry)

XX Human telomerase reverse transcriptase.

DE Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antinfertility; fungicide; antiparasitic;
KW antinflammatory; human; gene therapy.

OS Homo sapiens.

XX WO2003035667-A2.

XX 01-MAY-2003.

XX

PF 16-OCT-2002; 2002WO-US033065.
XX 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX (UYRP) UNIV ROCHESTER.
PA Rowley PT;
XX WPI; 2003-403336/38.
XX N-PSDB; ACC58039.
DR Novel double-stranded short interfering RNA having sense and antisense
DR nucleic acids which are complementary to each other and to target nucleic
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
PT transcriptase.
XX Disclosure; Fig 4; 37pp; English.
PS The present sequence is the protein sequence of human telomerase reverse
XX transcriptase (TERT). The invention relates to the discovery that double-
CC stranded interfering RNAs, such as short interfering RNAs (siRNA), which
CC target telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in anti-inflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWELVORGDPAAAFRALVACQVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWELVORGDPAAAFRALVACQVCVPW 60
Qy 61 DARPPPAAPFROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGAAGCPPEAFTTSVR 120
Db 61 DARPPPAAPFROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGAAGCPPEAFTTSVR 120
Qy 121 SYLPTNTVDALRGSGAWGALLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGALLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATOARPPPHASGPRRLGCRANVHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240
Db 181 ATOARPPPHASGPRRLGCRANVHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240
Qy 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVSPPARPAEATSLEGALSTRHSHPSVG 300
Db 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVSPPARPAEATSLEGALSTRHSHPSVG 300
Qy 301 RQHAGPPSTSRPPRMDTFCPPVYATKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPRMDTFCPPVYATKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGRSPPWPGTPRRLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPFLRAAVT 420
Db 361 VETIFLGRSPPWPGTPRRLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPFLRAAVT 420
Qy 421 PAAGVCAREKPGQSSVAAPPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSSVAAPPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFIISLGKHAHKLQELTWKMSVDRCAWLRRSPGVGCVPAAEHRLREEI 540

DB 481 RHNERFLRNTKFKTSLGKHAKLSQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
QY 541 LAKFLHLMMSVVVVELLSFFVTTTFQKNRLFFYKSVMSKLSIGIROHLKRVOLRE 600
DB 541 LAKFLHLMMSVVVVELLSFFVTTTFQKNRLFFYKSVMSKLSIGIROHLKRVOLRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVGLDDIHRAMWTFVLVRQAOPPPPELYFYKVDVTGAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVGLDDIHRAMWTFVLVRQAOPPPPELYFYKVDVTGAYDTI 720
QY 721 PQDLRLTEVIASIIKPONTYCVRRAVAVOKAAHGHVRKAFKSHVSTLTLQPYMRQFVAHL 780
DB 721 PQDLRLTEVIASIIKPONTYCVRRAVAVOKAAHGHVRKAFKSHVSTLTLQPYMRQFVAHL 780
QY 781 QETSPDRDAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPOGSILSTL 840
DB 781 QETSPDRDAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPOGSILSTL 840
QY 841 LCSLCYGD MENKLFAGIRDRGLLRLVDDFLLVTPHLLTHAKTFRTLVLRGVPYGCVVNL 900
DB 841 LCSLCYGD MENKLFAGIRDRGLLRLVDDFLLVTPHLLTHAKTFRTLVLRGVPYGCVVNL 900
QY 901 RKTVVNPFVEDEALGGTAFVOMPAGHLFPWCGLLDTRTLEVDSDSYSSYARTIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVOMPAGHLFPWCGLLDTRTLEVDSDSYSSYARTIRASLTF 960
QY 961 NRGFKAGNRMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLIQAAYRPHACVLQLP 1020
DB 961 NRGFKAGNRMRKLFVLRKCHSLFLDLQVNSLQTVCTNIYKILLIQAAYRPHACVLQLP 1020
QY 1021 PHQOVKNPTFFLRVISTASLCSYILKAKNAGMSLGAKGAAGPLPSEAVQWMLCHQAFLL 1080
DB 1021 PHQOVKNPTFFLRVISTASLCSYILKAKNAGMSLGAKGAAGPLPSEAVQWMLCHQAFLL 1080
QY 1081 KLTRHRYVYVPLGLSLRTAQTQLSRKLPGTTLTALEAANPALPSPDKTILD 1132
DB 1081 KLTRHRYVYVPLGLSLRTAQTQLSRKLPGTTLTALEAANPALPSPDKTILD 1132

RESULT 14
ABR42063
ID ABR42063 standard; protein; 1132 AA.
XX AC ABR42063;
XX AC ABR42063;
XX DT 28-JUL-2003 (first entry)
XX DE Human telomerase reverse transcriptase.
XX KW Telomerase reverse transcriptase.
XX KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
XX KW immunosuppressive; antiinfectility; fungicide; antiparasitic;
XX KW antiinflammatory; human; gene therapy.
XX OS Homo sapiens.
XX PN WO2003034985-A2.
XX PD 01-MAY-2003.
XX PF 16-OCT-2002; 2002WO-US033146.
XX PR 22-OCT-2001; 2001US-0345326P.
XX PR 20-FEB-2002; 2002US-0359196P.
XX PR 22-MAY-2002; 2002US-0383195P.
XX PA (UYRP) UNIV ROCHESTER.
XX XX

PI Rowley PT;
XX XX
DR WPI; 2003-403289/38.
DR N-PSDB; ACC57552.
XX XX
PT Novel nucleic acid encoding or comprising interfering RNAs which target
PT telomerase RNA, useful for inhibiting telomerase activity for treating
PT cancer, infertility and disorders of the immune system.
XX XX
PS Disclosure; Fig 4; 52pp; English.
XX XX
CC The present invention is that of human telomerase reverse transcriptase
CC (TERT). The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCAVRSLLSHSHYREVLPATFVRRLGPGQWRLVQRGDPAAAFALVAQCILVCVPM 60
DB 1 MPRAPRCAVRSLLSHSHYREVLPATFVRRLGPGQWRLVQRGDPAAAFALVAQCILVCVPM 60
QY 61 DARPPPAAPSFQVSCLEKELVARVQLRCERGAKNVLAFFGALLDGAAGGPEAFTTSVR 120
DB 61 DARPPPAAPSFQVSCLEKELVARVQLRCERGAKNVLAFFGALLDGAAGGPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGSSASRLPLPKRRR 240
DB 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGSSASRLPLPKRRR 240
QY 241 GAAPEPERTVQGSWAHPGTRGTPSDRGFCVSPARPABEATSLGALSCTRHSHPVG 300
DB 241 GAAPEPERTVQGSWAHPGTRGTPSDRGFCVSPARPABEATSLGALSCTRHSHPVG 300
QY 301 RQHAGPSTSRPRPMDTPCPVYAEYTKHFLYSSGDKQLRPSFLSSLPSTGARRL 360
DB 301 RQHAGPSTSRPRPMDTPCPVYAEYTKHFLYSSGDKQLRPSFLSSLPSTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFELIGNHAOCYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFELIGNHAOCYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQYVGFVACLRRLVPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQYVGFVACLRRLVPGLWGS 480
QY 481 RHNERFLRNTKFKTSLGKHAKLSQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
DB 481 RHNERFLRNTKFKTSLGKHAKLSQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
QY 541 LAKFLHLMMSVVVVELLSFFVTTTFQKNRLFFYKSVMSKLSIGIROHLKRVOLRE 600
DB 541 LAKFLHLMMSVVVVELLSFFVTTTFQKNRLFFYKSVMSKLSIGIROHLKRVOLRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660

Db 601 LSEAEVQHQREARFALLTSRLRFIPKPDGLRPIVNMDEVVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLGASVLGLDDIIRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLGASVLGLDDIIRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLQPMRQFVAHL 780
Db 721 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLQPMRQFVAHL 780
Qy 781 QETSPLRDVAVIEOSSLINEASSGLFDFVLFPMCHHVRIRGKSVYVOCQIGPOGSIILSTL 840
Db 781 QETSPLRDVAVIEOSSLINEASSGLFDFVLFPMCHHVRIRGKSVYVOCQIGPOGSIILSTL 840
Qy 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLLVTPHILTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLLVTPHILTHAKTFLRTLVRGVPEYGCVVNL 900
Qy 901 RKTVVNPFVEDEALGGTAFVOMPAGHLPFPWCGLLDDRTTLEVSQSDYSYARTSRASLTFF 960
Db 901 RKTVVNPFVEDEALGGTAFVOMPAGHLPFPWCGLLDDRTTLEVSQSDYSYARTSRASLTFF 960
Qy 961 NRGEKAGNRWRKLPGLVRLKCHSLFDLQVNSLOTCTNLYKTLLQLQAYRPHACVLQLP 1020
Db 961 NRGEKAGNRWRKLPGLVRLKCHSLFDLQVNSLOTCTNLYKTLLQLQAYRPHACVLQLP 1020
Qy 1021 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Db 1021 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Qy 1081 KLTRHRTVYVPLLGSRLTAQQLSRKLPFGTTLTALAAANPALPSDFKTLID 1132
Db 1081 KLTRHRTVYVPLLGSRLTAQQLSRKLPFGTTLTALAAANPALPSDFKTLID 1132

RESULT 15
ABP56676
ID ABP56676 standard; protein; 1132 AA.
XX
AC ABP56676;
XX
DT 25-MAR-2003 (first entry)
XX
DE Human telomerase reverse transcriptase protein SEQ ID NO:2
XX
KW Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
KW vulnary; antiulcer; epithelial cell migration promoter; wound;
KW epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
KW epithelial cell; keratinocyte; epidermal; mucosal.
XX
OS Homo sapiens.
XX
PN WO200291999-A2.
XX
PD 21-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014867.
XX
PR 09-MAY-2001; 2001US-0289903P.
XX
PA (GERO-) GERON CORP.
XX
PI Jiang X, Chiu C, Harley CB;
XX
DR WPI; 2003-120591/11.
DR N-ESDB; ABZ22474.
XX
PT Composition for treating wounds and enhancing epithelization of a skin
PT surface, comprises vector encoding telomerase reverse transcriptase or
PT telomerized epithelial cells on a microparticle or a matrix.
XX
PS Disclosure; Page 32; 68pp; English.
XX

CC The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomerase epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnerary and antiulcer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelisation of a skin surface. The wound is especially skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence represents human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5
XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWRLVQGDPAAFRALVQAQLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWRLVQGDPAAFRALVQAQLVCVPM 60
Qy 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGALLDARGGPEAFTTSVR 120
Qy 121 SYLPTNTVTDALRGSGAWGLLRLRVGDDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVTDALRGSGAWGLLRLRVGDDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRLSLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRLSLPKRPRR 240
Qy 241 GAPEPERTVQGGSWAHPORTGSDRGFCVSPAPABEATSEALSGSTRHSHPVS 300
Db 241 GAPEPERTVQGGSWAHPORTGSDRGFCVSPAPABEATSEALSGSTRHSHPVS 300
Qy 301 RQHHAGPPSTSRPPRPMWDTPCPVYAEKHFVLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Db 301 RQHHAGPPSTSRPPRPMWDTPCPVYAEKHFVLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSREPMFCTPRRLPRLPQRYWQMRPLFLELGNHAQCYPGYLLKTHCFLRAVT 420
Db 361 VETIFLGSREPMFCTPRRLPRLPQRYWQMRPLFLELGNHAQCYPGYLLKTHCFLRAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSFPWQYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSFPWQYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERRELNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRSPSGVCPVAAEHLREEI 540
Db 481 RHNERRELNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRSPSGVCPVAAEHLREEI 540
Qy 541 LAKFLHLMVYVVELLSRFFYVTTTFFQKRLFFYRKSVMKLSQSIGIRQHLKRVQURE 600
Db 541 LAKFLHLMVYVVELLSRFFYVTTTFFQKRLFFYRKSVMKLSQSIGIRQHLKRVQURE 600
Qy 601 LSAEVRQHQREARFALLTSRLRFIPKPDGLRPIVNMDEVVVGARTFRREKRAERLTSRVKA 660
Db 601 LSAEVRQHQREARFALLTSRLRFIPKPDGLRPIVNMDEVVVGARTFRREKRAERLTSRVKA 660

Qy	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI	720
Db	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI	720
Qy	721	PODLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL	780
Db	721	PODLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL	780
Qy	781	QETSPLRDAVVIEOSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOGSIILSTL	840
Db	781	QETSPLRDAVVIEOSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOGSIILSTL	840
Qy	841	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900
Db	841	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900
Qy	901	RKTVVNPFVEDEALGGTAFVOMPAGLFPWCGLLLDTRTLEVOSSYSSYARTSIRASLTF	960
Db	901	RKTVVNPFVEDEALGGTAFVOMPAGLFPWCGLLLDTRTLEVOSSYSSYARTSIRASLTF	960
Qy	961	NRGFKAGRNMRKLFGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020
Db	961	NRGFKAGRNMRKLFGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020
Qy	1021	FHQQVWKNPTFFFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080
Db	1021	FHQQVWKNPTFFFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080
Qy	1081	KLTRHRVTVYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD	1132
Db	1081	KLTRHRVTVYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD	1132

Search completed: January 10, 2005, 17:34:53
Job time : 175 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 17:22:50 ; Search time 215 Seconds
(without alignments)
3029.414 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPRAPRCRAVRLSRHRE.....TALEAAANPALPSDFKTLTD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5961	100.0	1132	1	TERT_HUMAN	Q14746 homo sapien
2	5583.5	93.7	1069	2	Q8NG46	Q8ng46 homo sapien
3	4052	68.0	807	2	Q8N6C3	Q8n6c3 homo sapien
4	3973	66.6	795	2	Q8NG38	Q8ng38 homo sapien
5	3628	60.9	1128	2	Q8QX24	Q8qx24 mesocricetu
6	3505	58.8	1122	1	TERT_MOUSE	Q70372 mus musculus
7	2825	47.4	524	2	Q9UBR6	Q9ubr6 homo sapien
8	2590	43.4	1346	2	Q6RD80	Q6rd80 gallus gall
9	2590	43.4	1346	2	AA575793	AA575793 gallus ga
10	2316.5	38.9	1191	2	Q9DE32	Q9de32 xenopus lae
11	2207.5	37.0	523	2	Q94807	Q94807 homo sapien
12	2016	33.8	575	2	Q9JK99	Q9jk99 rattus norv
13	1373	23.0	514	2	Q9R266	Q9r266 mus musculus
14	724.5	12.2	1123	2	Q9SE39	Q9se99 arabidopsis
15	724.5	12.2	1123	2	Q9SPU7	Q9spu7 arabidopsis
16	688	11.5	1259	2	Q9AUI3	Q9aul3 oryza sativ
17	654.5	11.0	1261	2	Q8LKW0	Q8lkw0 oryza sativ
18	594	10.0	988	1	TERT_SCHPO	Q13339 schizosacch
19	478	8.0	1032	2	Q7Z1L1	Q7z1l1 euplotes cr
20	474	8.0	1032	2	Q8MUB3	Q8mub3 euplotes cr
21	469.5	7.9	939	2	Q7SD71	Q7sd71 neurospora
22	450	7.5	85	2	Q8UNS6	Q8uns6 homo sapien
23	450	7.5	940	2	Q8C9D0	Q8c9d0 yarrowia li
24	449	7.5	116	2	Q8OSU5	Q8osu5 rattus norv
25	448.5	7.5	1031	1	TERT_EUPAE	Q00939 euplotes ae
26	441	7.4	1032	2	Q7Z1L0	Q7z1l0 euplotes cr
27	408	6.8	823	2	Q8SQ00	Q8sq00 encephalito
28	397	6.7	104	2	Q8JLM1	Q8jlm1 mus musculus
29	395.5	6.6	1135	2	Q8I8Z7	Q8i8z7 sterkiella
30	395	6.6	1132	1	TERT_OXYTR	Q76332 oxytricha t
31	395	6.6	1132	2	AA87865	AA87865 sterkiell

32 394 6.6 73 2 Q9UNR4 Q9unr4 homo sapien
33 392 6.6 1108 2 Q8I8Z6 Q8i8z6 sterkiella
34 389.5 6.5 861 2 Q6CS0 Q6cs0 kluyveromyc
35 365 6.1 867 2 Q9P8T3 Q9p8t3 candida alb
36 364 6.1 895 2 Q9GRCS Q9grcs paramecium
37 363 6.1 1117 1 TERT_TETH TERT_TETH
38 361 6.1 867 2 Q9P8T2 Q9p8t2 candida alb
39 356.5 6.0 884 1 TERT_YEAST Q6L163 saccharomyc
40 355.5 6.0 894 2 Q6BUF6 Q6buf6 debaryomyc
41 342 5.7 896 2 Q8MUQ8 Q8muq8 paramecium
42 339 5.7 79 2 Q7YR69 Q7yr69 felis silve
43 338 5.7 79 2 Q76K45 Q76k45 canis famil
44 338 5.7 79 2 BAD06179 Bad06179 canis fam
45 320 5.4 853 2 Q752S9 Q752s9 ashbya goss

ALIGNMENTS

RESULT 1

ID TERT_HUMAN STANDARD; PRT; 1132 AA.
AC O14746: O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HST12) (Telomerase-associated protein 2) (TP2).
DE subunit) (HST12) (Telomerase-associated protein 2) (TP2).
GN Name=TERT; Synonyms=TRT, EST2, TCS1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney; PubMed=9252327;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97433088; PubMed=9288757;
RA Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q., Bacchetti S., Haber D.A., Weinberg R.A.;
RT "hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization."; Cell 90:785-795 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99267414; PubMed=10333526;
RA Wick M., Zubov D., Hagen G.;
RT "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)."; Gene 232:97-106 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene."; Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION IN TELOMERASE ACTIVITY, TISSUE SPECIFICITY, ASSOCIATION WITH TERT1, AND MUTAGENESIS OF ASP-868; ASP-869 AND ASP-712.
RX PubMed=9389643;
RA Harrington L., Zhou W., McPhail T., Oulton R., Yeung D.S., Mar V., Bass M.B., Robinson M.O.;
RT "Human telomerase contains evolutionarily conserved catalytic and structural subunits."; Genes Dev. 11:3109-3115 (1997).
RN [6]
RP ASSOCIATION WITH TERT1.

```

RX PubMed=11029039;
RA Beattie T.L., Zhou W., Robinson M.O., Harrington L.;
RT "Polymerization defects within human telomerase are distinct from
RL telomerase RNA and TEPI binding.";
RL Mol. Biol. Cell 11:3329-3340(2000).
CC -1- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -1- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
CC least composed of TEPI, EST1A, POT1 and a telomerase RNA template
CC component (TER). Interacts with PINX1.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: Activation and cancer cell pathogenesis.
CC immortalization and cancer cell pathogenesis.
CC -1- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@sib-ebi.ch).
CC -----
DR EMBL; AF015950; AAC51672.1; -.
DR EMBL; AF018167; AAC51724.1; -.
DR EMBL; AF128894; AAB30037.1; -.
DR EMBL; AF128893; AAB30037.1; JOINED.
DR EMBL; AY007685; AAC23289.1; -.
DR PIR; T03844; T03844.
DR Genew; HGNC:11730; TERT.
DR MIM; 187270; -.
DR GO; GO:000781; C:chromosome, telomeric region; TAS.
DR GO; GO:0042162; F:telomeric DNA binding; TAS.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; TAS.
DR InterPro; IPR000477; RTase.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-binding; Nuclear protein; Ribonucleoprotein;
DR RNA-directed DNA polymerase; Telomere; Transferrase.
FT MUTAGEN 868 868 DD->AA: Loss of telomerase activity.
FT MUTAGEN 869 869 DD->AA: Loss of telomerase activity.
FT MUTAGEN 712 712 D->A: Loss of telomerase activity.
FT MUTAGEN 516 516 D -> G (in Ref. 2).
FT CONFLICT 516 516 D -> G (in Ref. 2).
SQ SEQUENCE 1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;

Query Match 100.0%; Score 5961; DB 1; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGQWRLVQGDPAAFRALVAQCLVCVPW 60
DB 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGQWRLVQGDPAAFRALVAQCLVCVPW 60
QY 61 DARRPPAAPSPFQVSCIKELVARVLQRLCERGAQNVLAFAFALLDARGGPPFAFTSVR 120
DB 61 DARRPPAAPSPFQVSCIKELVARVLQRLCERGAQNVLAFAFALLDARGGPPFAFTSVR 120
QY 121 SYLPNTVTDLRSGGAWGLLRVGGDVLVHLLARCAFLVLPAPSCAYQVCGPPLVOLGA 180
DB 121 SYLPNTVTDLRSGGAWGLLRVGGDVLVHLLARCAFLVLPAPSCAYQVCGPPLVOLGA 180
QY 181 ATQARPPPHASGPRRLGCRANVHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 240
DB 181 ATQARPPPHASGPRRLGCRANVHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 240
QY 241 GAAPERTPTVPGQGSWAHPQRTGPDGRFCVVPSPARPABEATSLGALSGTRHSPSVG 300

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DB 241 GAAPERTPTVPGQGSWAHPQRTGPDGRFCVVPSPARPABEATSLGALSGTRHSPSVG 300
QY 301 RQHAGPPTSRPRPDPWDTPCPVYAEATHFLYSSGDKQQLRPSFLLSLRPSLTGARRL 360
DB 301 RQHAGPPTSRPRPDPWDTPCPVYAEATHFLYSSGDKQQLRPSFLLSLRPSLTGARRL 360
QY 361 VETIFLGSRPWMEGTTPRRLPRLPQRYWQMRPLELLELGNHAQCPYGVLLKTHCPRAAVT 420
DB 361 VETIFLGSRPWMEGTTPRRLPRLPQRYWQMRPLELLELGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVAREKPKQGSVAAPBEEDTDPRLVOLLRQHSPPWQVYGFVRACLRRLLVPPGLWGS 480
DB 421 PAAGVAREKPKQGSVAAPBEEDTDPRLVOLLRQHSPPWQVYGFVRACLRRLLVPPGLWGS 480
QY 481 RHNERFLPNTKKFISLGKHAHKLQELTWKMSVRDCAMLRSPGVCVGAASRRLREEI 540
DB 481 RHNERFLPNTKKFISLGKHAHKLQELTWKMSVRDCAMLRSPGVCVGAASRRLREEI 540
QY 541 LAKFLHMLMSVYVVELLRSPFFVYVTTTFQKNRFFYRKSVWSKLQSIGIRQHLLKRVQRE 600
DB 541 LAKFLHMLMSVYVVELLRSPFFVYVTTTFQKNRFFYRKSVWSKLQSIGIRQHLLKRVQRE 600
QY 601 LSEAEVQREHREARPAALLTSRLRFIPKPDGLRPTVNNDYVVGARTFRREKRAERLTSRKA 660
DB 601 LSEAEVQREHREARPAALLTSRLRFIPKPDGLRPTVNNDYVVGARTFRREKRAERLTSRKA 660
QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRFKSHVSTLTLDLPYMRQFVAHL 780
DB 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRFKSHVSTLTLDLPYMRQFVAHL 780
QY 781 QETSPLRDADVIEQSSSLNEASGLDFVFLRPMCHHVRIRGKSVYVQCGIPGSGILSTL 840
DB 781 QETSPLRDADVIEQSSSLNEASGLDFVFLRPMCHHVRIRGKSVYVQCGIPGSGILSTL 840
QY 841 LCSLCYGDMEKLFAGIRDDGLLLRLVDDDFLAVTPLHAKTFLRTLVRGVPYGCVVNL 900
DB 841 LCSLCYGDMEKLFAGIRDDGLLLRLVDDDFLAVTPLHAKTFLRTLVRGVPYGCVVNL 900
QY 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTLRTLEQSDYSSVARTSIRASLTF 960
DB 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTLRTLEQSDYSSVARTSIRASLTF 960
QY 961 NRGFKAGRNMRKLFQVLRBLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFKAGRNMRKLFQVLRBLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHOQVWKNPTFFLVRISDTASLCYSILKAKNAGMSLGAKAGPLPSEAVQWLCHOAFL 1080
DB 1021 FHOQVWKNPTFFLVRISDTASLCYSILKAKNAGMSLGAKAGPLPSEAVQWLCHOAFL 1080
QY 1081 KLTRHRTVTVPLGLSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRTVTVPLGLSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 2
Q8NG46 PRELIMINARY; PRT; 1069 AA.
ID Q8NG46;
AC Q8NG46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
DE Name=HTRT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RA Hiseatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085628; BAC11010.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1069 AA; 120046 MW; BE1E77A653B1C666 CRC64;

Query Match 93.7%; Score 5583.5; DB 2; Length 1069;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 0; Indels 63; Gaps 1;

Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQGDPAAPRALVAQCLVCVPW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQGDPAAPRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFAFGFALLDGGAGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFAFGFALLDGGAGGPPPEAFTTSVR 120

Qy 121 SYLENTVTDALRGSGAWGLLRLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLENTVTDALRGSGAWGLLRLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGPRRRLLGGERAWNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240
Db 181 ATQARPPPHASGPRRRLLGGERAWNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240

Qy 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSILEGALSGTRHSHPSVG 300
Db 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSILEGALSGTRHSHPSVG 300

Qy 301 RQHAGPPSTSRPPMDTPCPVYAEETHFLYSSGDKQELRPSFLSSLSPLSTGARRL 360
Db 301 RQHAGPPSTSRPPMDTPCPVYAEETHFLYSSGDKQELRPSFLSSLSPLSTGARRL 360

Qy 361 VETIFLGSRPMPGTPRRLLPRLPORYQWQMRPLFELIGNHAQCPYGVLLKTHCPLEAAVT 420
Db 361 VETIFLGSRPMPGTPRRLLPRLPORYQWQMRPLFELIGNHAQCPYGVLLKTHCPLEAAVT 420

Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSHSPWQYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSHSPWQYGFVRACLRLVPPGLWGS 480

Qy 481 RHNERRRFLRNTKFTISLGKHAQLSLQELTWQMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRRFLRNTKFTISLGKHAQLSLQELTWQMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy 541 LAKFLHLWMSVYVVELLRSPYVTTTFQKNRLLFFYRKSVMSKLQSIGIRHLKRVQLRE 600
Db 541 LAKFLHLWMSVYVVELLRSPYVTTTFQKNRLLFFYRKSVMSKLQSIGIRHLKRVQLRE 600

Qy 601 LSEAEVQRHREARFALLTSRLRFTPKPDGLPIVNDYVVGARTFREKRAERLTSRYKA 660
Db 601 LSEAEVQRHREARFALLTSRLRFTPKPDGLPIVNDYVVGARTFREKRAERLTSRYKA 660

Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFFVLVRAQDPPPELVPKVDVDTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFFVLVRAQDPPPELVPKVDVDTGAYDTI 720

Qy 721 QDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
Db 721 QDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780

Qy 781 QETSPRLDAVVEOSSSNEASSGLFDVFLRPMCHAVRIRGKSVYQCQGIPOQSII STL 840
Db 781 QETSPRLDAVVEOSSSNEASSGLFDVFLRPMCHAVRIRGKSVYQCQGIPOQSII STL 840

Qy 841 LCSLCYGDMMENKULFAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGDMMENKULFAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFL----- 884

Qy 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSYASRTSIRASLTF 960
Db 885 -----SYARTSIRASLTF 897

Qy 961 NRGFKAGRNMRRLFGVRLRKCHSLFDLDQVNSLQTVCTNIIKLLQAYRFHACVLQLP 1020
Db 898 NRGFKAGRNMRRLFGVRLRKCHSLFDLDQVNSLQTVCTNIIKLLQAYRFHACVLQLP 957

Qy 1021 FHOQVKNPFTFLRAVISDTASLCYSILKAKNAGNSLGAAGAGPLPSEAVQWLCHQAFLL 1080
Db 958 FHOQVKNPFTFLRAVISDTASLCYSILKAKNAGNSLGAAGAGPLPSEAVQWLCHQAFLL 1017

Qy 1081 KLTHRRVTVPLLGSLRTAQTQLSRKLPGTTTLTALEAAANPALPSDFKTILD 1132
Db 1018 KLTHRRVTVPLLGSLRTAQTQLSRKLPGTTTLTALEAAANPALPSDFKTILD 1069

RESULT 3

Q8N6C3 PRELIMINARY; PRT; 807 AA.

ID Q8N6C3 AC Q8N6C3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta and gamma deletion isoform of telomerase reverse transcriptase.
DE transcritpase.
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUS=Gastric cancer;
RA Hiseatomi H., Nagao K., Kanamaru T., Sumida H., Hirata H., Yamamoto M.,
RA Kazumasa H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086379; BAC11014.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 807 AA; 90225 MW; 199664460CE6D763 CRC64;

Query Match 68.0%; Score 4052; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 9e-245;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQGDPAAPRALVAQCLVCVPW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQGDPAAPRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFAFGFALLDGGAGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFAFGFALLDGGAGGPPPEAFTTSVR 120

Qy 121 SYLENTVTDALRGSGAWGLLRLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLENTVTDALRGSGAWGLLRLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGPRRRLLGGERAWNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240
Db 181 ATQARPPPHASGPRRRLLGGERAWNHSVREAGVPLGLPAGARRRGGSGASRSLPLPKPRR 240

Qy 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSILEGALSGTRHSHPSVG 300
Db 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSILEGALSGTRHSHPSVG 300

DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128393 MW; 1D4F81249012174E CRC64;

Query Match 60.9%; Score 3628; DB 2; Length 1128;

Best Local Similarity 63.3%; Pred. No. 4.5e-218; Mismatches 239; Indels 64; Gaps 16;

Matches 736; Conservative 124; Mismatches 239; Indels 64; Gaps 16;

QY 1 MPAPRCRAVRSLLRSRYREVLPLATFVRRLLPGQWRLVORGDPAAAFRALVAQCLVCVPW 60

DB 1 MPAPRCRAVRSLLRSRYREVLPLATFVRRLLPGQWRLVORGDPAAAFRALVAQCLVCVPW 60

QY 61 DARPPAPSPROVSCLELVARVLRORLCERGAKNVLAFLDAGRGPPAFTTSVR 120

DB 61 DSQPPADLSFHQVSSLSKELVARVVRQLCERGNVLTFFGALLNGAQQGPPMTFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLRRYDGDVLLHLLARCALFVLVAPSCAVQVCGPPLXOLGA 180

DB 121 SYLNSVTVESURVSGAMLLNRVGDLLVLLARCALYLLVPPSCAYQVCGSPLYQICA 180

QY 181 ATQARPP-PHASGRRRLG-----CERAWNSVREAGVPLGLPAPARRRGCSASRS 231

DB 181 TAETWPSVSRVYRTPRGVNFTHLGSVTHRVNSHQEAWKPPPLPSREAKRSLSITNRS 240

QY 232 LPLPKRPRRGAAPERTPVQGGWAHPGRTGRGSDRGFCVVSAPAR-----PAEBATSLG 287

DB 241 VPPSKARCDLAPRLKGPYRQA-----VPTPSDKTW-VPNPAKSHAVPISRTTK-ED 291

QY 288 ALSGTRHSHPSVGRQ----HAGPST-S-RP-----RPWTPCPVVAETKHYLS 334

DB 292 LSSGVK--APGLSRSGSVCYKHKPSSTLSQSPLCNAPQLRP-----YTETKRFYS 341

QY 335 -SGDKEQLRPSFLSSRLPSLTGARRLVETTFILGSRPMPGTPRRLLRPLORYQWMPPLF 393

DB 342 REGGRNLNPSFLNNLPSLTGARRLVETTFILGSRPMPGTPRRLLRPLORYQWMPPLF 401

QY 394 LELGNAQCYPYVLLKTHCPRLAAVTPAAGVCAAREKPPQGSVAAPBEDTDPRLVOLLR 453

DB 402 QQLLVNARCPYVLLRSHCFRTAAHQVAGAL-----NTTSPQLMNLRL 447

QY 454 QHSSPWQYGVFRACRLRLVPPGLWGNHRRFLNRTKFKFISLQKAKLSLQBLTWMS 513

DB 448 LHSSPWQYGVFRACRLRLVPPGLWGNHRRFLNRTKFKFISLQKAKLSLQBLTWMS 507

QY 514 VRDCAWLRSPGVGCPVAAEHLREEILAKFLHLMSSVYVVELLSPPYVTETTFQKNRL 573

DB 508 VQDCWLRSPGVGCPVAAEHLREEILAKFLHLMSSVYVVELLSPPYVTETTFQKNRL 567

QY 574 FFYKSVMSKLSQIGIOHLKRVQLRELSEAVRQHRREARPALTSRLRFLPKPDGLRPI 633

DB 568 FFYKSVMSKLSQIGIOHLKRVQLRELSEAVRQHRREARPALTSRLRFLPKPDGLRPI 627

QY 634 VMDDYVVGARTFREKRAERLTSRKALFSLVNLTERARRPGLGASVLGLDDIIRAWRTF 693

DB 628 VMMSY-MGTRAPDFRKGQAQHPFQCLKTLFSLVNLTERARRPGLGASVLGLDDIIRAWRTF 686

QY 694 VLVRADQPPPELYFVKVDVTVGADVTIPQDLRLTEVIASLIK-PONTYCVRYAVVOKAAH 752

DB 687 VLVRADQPPPELYFVKVDVTVGADVTIPQDLRLTEVIASLIK-PONTYCVRYAVVOKAAH 746

QY 753 GHVRKAFKSHVSTLTDLPYVMRQFVAHLQ--ETSPLRDAVIEQSSSNEASSGLFDVFL 810

DB 747 GQIHKSFRQVSTLSDLOPHMGQFLKHLQDSDTBALNSVVEQSLNEASSSLEFFFL 806

QY 811 RFMCHAVIRKGSYVQCGQIPQGSILSTLCSLCYGDMMENKLPAGIRRDGLLRVDDF 870

DB 807 RFVRNSVVKIGRCVQVQCGQIPQGSILSTLCSLCYGDMMENKLPAGIRRDGLLRVDDF 866

QY 871 LLVTPHLTHAKTFLRTLVRGVPEYGVVNLKTKTVNPFVDEALGGTAFVQMPAHGLPPW 930

DB 867 LLVTPHLVQAEAFRALVRGIPEYGCMLNLTQTVNPFVDEALGGTAFVQMPAHGLPPW 926

QY 931 CGLLDTRTLEVSQSYARTSTRASITFNRGFKAGNMRKLFGLVRLKCHSLFLDLQ 990

DB 927 CGLLDTRTLEVSQSYARTSTRASITFNRGFKAGNMRKLFGLVRLKCHSLFLDLQ 986

QY 991 VNSLQTVCTNIYKILLQAVRFHACVQLQPLPHQOVWKNPTFFLRVISTASLCYSILKAK 1050

DB 987 MNSLQTVCTNIYKILLQAVRFHACVQLQPLPHQOVWKNPTFFLRVISTASLCYSILKAK 1046

QY 1051 NAGSLGAKGAGPLPSEAVQWLCHQAPFLKLTTHRVTVYVPLGLSLRTAQTLGRKLPGT 1110

DB 1047 NAGMTLAKGAGSGFPPEAARWLCYQAFLLKLAGHSVTKCLGLPLRTAQQLCKRLPRA 1106

QY 1111 TLTALEAANPALPSDFKTILD 1132

DB 1107 TMAILEAADPALSTDFQTILD 1128

RESULT 6

TERT_MOUSE
ID TERT_MOUSE STANDARD; PRT; 1122 AA.
AC 070372; O35432;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
GN Name=Tert;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98241176; PubMed=9582020;
RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
RT "Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation.";
RL Oncogene 16:1723-1730(1998).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=98393668; PubMed=9724727;
RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
RT "Expression of mouse telomerase catalytic subunit in embryos and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
RN (3)
RP SEQUENCE OF 550-616 FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Partial sequence of Mus musculus telomerase catalytic subunit homolog.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at least composed of TEP1, EST1A, POT1 and a telomerase RNA template component (TER). Interacts with PINX1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family. Telomerase subfamily.

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Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRVLVQRGDDPAAFRALVAQCLVCVPW	60
Db	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRVLVQRGDDPAAFRALVAQCLVCVPW	60
Qy	61	DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR	120
Db	61	DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR	120
Qy	121	SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA	180
Db	121	SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA	180
Qy	181	ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR	240
Db	181	ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR	240
Qy	241	GAAPERTPVQGSWAHPGTRGSDRGFCVWSPARPAEBATSLGALSCTRSHSPSVG	300
Db	241	GAAPERTPVQGSWAHPGTRGSDRGFCVWSPARPAEBATSLGALSCTRSHSPSVG	300
Qy	301	ROHAGPSTSRPRPMDTPCPVYAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL	360
Db	301	ROHAGPSTSRPRPMDTPCPVYAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL	360
Qy	361	VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPVGVLLKTHCPRAAVT	420
Db	361	VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPVGVLLKTHCPRAAVT	420
Qy	421	PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSPPWQVYGFVRACLRRLVPPGLWGS	480
Db	421	PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSPPWQVYGFVRACLRRLVPPGLWGS	480
Qy	481	RHNERFLRNTKFKISLGKHAQLSLQELTWQMSVRDCAWLRRSP	524
Db	481	RHNERFLRNTKFKISLGKHAQLSLQELTWQMSVRDCAWLRRSP	524
RESULT 8			
Q6RD80			
ID	Q6RD80; PRELIMINARY; PRT; 1346 AA.		
AC	Q6RD80;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Telomerase reverse transcriptase.		
GN	Name=TER1;		
OS	Gallus gallus gallus.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=208526;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Delany M.E., Daniels L.M.;		
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY502592; AAS75793.1; -		
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.		
DR	InterPro; IPR003545; Telomerase_RT.		
DR	PRINTS; PR01365; TELOMERASRT.		
KW	RNA-directed DNA polymerase.		
SQ	SEQUENCE 1346 AA; 155316 MW; E93A8B64FB6A4D40 CRC64;		
Query Match 43.4%; Score 2590; DB 2; Length 1346;			
Best Local Similarity 44.1%; Pred. No. 4.5e-153;			
Matches 593; Conservative 159; Mismatches 350; Indels 242; Gaps 29;			
Qy	9	AVRSLRSHYREVLPLATFVRRL--GPGQWRVLVORGDDPA-AFRALVAQCLVCVPWDARPP	65
Db	25	AVLGALRGYCAEXTPLFAFVRLRQEGGTGEVRLRGDDAQCYRTFVSCVVCVPRGARAI	84
Qy	66	PAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVRSYLPN	125

Db	85	PRPICFOQLSSQSEVITRIVQRLCEKKKNLILAYGSLDENSCHFRVLPSSCIYSYLSN	144
Qy	126	TVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGNATQAR	185
Db	145	TVTETIRISGLWEILLRIGDDVMYLLHLCALFVLVPPSNICYVCGQPIYEL--TSRNVG	203
Qy	186	PPP-----HAS---GPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASR-	230
Db	204	PSPGFVRRYSRFXHNSLLDYVRKLVFHR---HYLSKSWMKCRP-----RRGRVSSRR	256
Qy	231	-----SLPLP-----KRPRGAA	243
Db	257	KRRSHRISQLRSGYQPSAKVNFQARQISTVTARLEKQSCSSCLCLPARAPSLKRKRDEQ	316
Qy	244	PE-----PERTPVGGG-----SW-----	256
Db	317	VEITAKRVKMEKEIERQACISIVPD---VNSSQRHGTSWHVAPRAVGLIKHEYISERS	373
Qy	257	-----AHPGR-----TRG-----	264
Db	374	NSEMSGPSVHRSHPGKRPVADKSSFQGVQGNKRIKTGAEKRAESNRGIEMYINPIHK	433
Qy	265	PSDRGP-CVVSPPAPAE-----EATSEALGSGTRHSHPSVGRQHHAGGPSTSRPPRWD	319
Db	434	PNRRGIERRINPTHKPELNSVQTEPMEGASSGDRKQE-----NPPAHLAKQLPNTL	484
Qy	320	PCPPVYAETKHFYSSGDKQLRPSFLSSLRPSLTGARRLVETIFLGSRPW-----M	372
Db	485	SRSVTYFEKPLLSYRSYQYFPKSFILSRLOCGQAGRRLIETIFUSQNPKEQOQNSL	544
Qy	373	PGTPRRRLPRLPORYWQMRPLFLELLGNHAQCPVGVLLKTHCP-----LRAA	418
Db	545	POQWRKRLPKRWQMRREIFQKLVKNHEKCPYLVLKNCPCVLLSEACLKKTTLTLOAA	604
Qy	419	VTAAAGV-----CAREKPG-----SVAA---PEE-----EDTDPRRLVQLLRQ	454
Db	605	LPGEAKVHKTEHGKSTEGTAPNSFLAPPSVLACGQPERGEQHPAESDP--LLRELLRQ	663
Qy	455	HSSPWQVYGFVRACLRRLVPPGLWGRHNERFRNTKFKISLGKHAQLSLQELTWKMSV	514
Db	664	HSHWQVYGFVRECLREVI PAELWGSSHNKCRFFKNVKAFISMKGAKLSLQQLMKMRV	723
Qy	515	RDCAWLRRSPGVCVPAAEHRLREILAKFLHMLMSVYVVELLSRFFVVTETTFOKNRLF	574
Db	724	NDCVWLAKGNHSPVAYEHCYREILAKFLYWLMDSVYIELLSKFFVITETMQKMLF	783
Qy	575	PYRKSVMKLSQSIGIROHLKRVQLRELSAEFVROHREARPALTSRLRFIPKPDGLRPV	634
Db	784	YRKFVWGLQNGIRDFHFAKVLHRLALSSEMEVIRQKYPPIASRLRFIPKMGRLRPV	843
Qy	635	NMDYVVGARTF---RREKRAERLTSRVKALFSLVNYERARRPGLLGASVLGDDIHRAR	691
Db	844	RLSRVBEQKLSKESREKKIQRVNTQKLNFLSVLNYERTVNTSIGSVFGRDDIYRKWK	903
Qy	692	TFVLRV-RAQDPPPELVFVVDVTGAYDTTPODRLTEVIAIIXP--QNTVCVRYAVVQ	748
Db	904	EFVTKVFESGEMPHFYPVKGDSVRADFTTIPHKLVLEVISQVLKPESQTVYGIWYAVIM	963
Qy	749	KAAGHVRKAPKSHVSTLTDLPQYMRQFVAHLQETSPLRDVAVTEQSSSLNEASSGLPDV	808
Db	964	ITPTGKARKLYKXHVSTFDFIPDMKQFVSKLQERTSLRNAIVVEQCLTFNENSSTLPTF	1023
Qy	809	FLRFMCHHAVRIGKSVVQCGIPQSGISLTLLCSLCYGMENKLFAGIRRDGLLLRLVD	868
Db	1024	FLQMLHNLIEIGHRYIQCSIGIPQSGISLTLLCSLCYGMENKLLCGIQKQDGLVIRLID	1083
Qy	869	DELLVTPHLTHAKTFLATLVRGVPYCVNLRKTVNFPVEDEALGTAFAVQPAHGLF	928
Db	1084	DFLLVTPHLMQARTFLRTIAGIPEYGFLLINAKKTVNFPV-DDIPGSKFKHLPDCRLI	1142
Qy	929	PWCGLLDTTLEVSQSDYSYARTSIRASLTFRNGFKAGRNMRKLFVGLRLKCHSLFLD	988

Db 1143 SMCGLLDVQTLLEVYCDYSSAFTSIRSSLSFNSRIAGKNNCKLTAVLKLKCHPLLLD 1202
QY 989 LOVNSLQVCTNVIYKILLQAYRFHACVQLQLPFHQVWKNPFFFLRVISDTASLCYSILK 1048
Db 1203 LKINSLOTVLINIKYIFLLQAYRFHACVQLQFPNQVRNPDFFLRISDTASCCYFLK 1262
QY 1049 AKNAGMSLGAAGAAGPLPSEAVQWLCHOAFLLKLTTRHVVYVPLIGSLRTAQOLSRKLP 1108
Db 1263 AKNPGVSLGSKDASGMFFPEAAEWLCYHAFIVKLSNKHVYKCLLKPLKYVMHFLGKIP 1322
QY 1109 GTTLTALAAANPALPSPDKTILD 1132
Db 1323 RDTMELLKTVTEPSLCQDFKTILD 1346
RESULT 9
AAS75793
ID AAS75793 PRELIMINARY; PRT; 1346 AA.
AC AAS75793;
DT 31-MAR-2004 (TremBLrel. 27, Created)
DT 31-MAR-2004 (TremBLrel. 27, Last sequence update)
DE Telomerase reverse transcriptase.
GN TERT.
OS Gallus gallus gallus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus; Gallus gallus.
OX NCBI_TaxID=208526;
RN [1]
RP
RA Delany M.E., Daniels L.M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY502592; AAS75793.1; --
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1346 AA; 15316 MW; E93A8B64FB6A4D40 CRC64;

Query Match 43.4%; Score 2590; DB 2; Length 1346;
Best Local Similarity 44.1%; Pred. No. 4.5e-153;
Matches 593; Conservative 159; Mismatches 350; Indels 242; Gaps 29;

QY 9 AVRSLLRSHYREVLPLATFVRL--GPGWRLVORGDA-AFRALVAQCLVCPWDARPP 65
Db 25 AVLGAALRGYAEVTPLEAFVRLLEGGTGEVLRGDDAQCRTFVSQCVCVPRGARAI 84
QY 66 PAAPSFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGAAGPPEATTSSVRSYLPN 125
Db 85 PRPICFQQLSQSQSEVITRIVQRLCEKKKNILAYGSLDENSCHPVLPSSCIYSYLSN 144
QY 126 TVTDALRGSGAWGLLRGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQAR 185
Db 145 TVTETIRISGLWEILLRIGDDVMYLLHLCALFMLVPPSNQVQCQPIYEL-ISRNVG 203
QY 186 PPP-----HAS---GPRRLCERAWNHSVREAGVPLGLPAGARRGGGSASR- 230
Db 204 PSPGFVRRYRSFRKHSNLLDYVRKLVFHR---HYLSKQWMKCRP-----RRRGVSSRR 256
QY 231 -----SLPLP-----KRPRGAA 243
Db 257 KRRSHRTQSLRSGYQPSAKVNFQNGROIISTVTARLEKQSCSSLCPLPARPSLKRKRDEQ 316
QY 244 PE-----PERTPVQGG-----SW----- 256
Db 317 VEITAKRVKIMEKEIEBQACISVPD---VNQSSQRHGTSWHVAPRAVGLIKEHYISERS 373
QY 257 -----AHPGR-----TRG----- 264
Db 374 NSEMSGVSVHRHFGKRFVADKSSFPQVQGNKRIKTGAEKRAESNRGRIEMYINPIHK 433
QY 265 PSDRGF-CVVSPPARPAE-----EATSLGALSGTRHSHPSVGRQHHAGPPSTSRPPMDT 319
Db 434 PNRRIERRINPTHKPELNSVQTEPMEGASSGDRKQE-----NPAHLAKQLPNTL 484

QY 320 PCPVPVYAEKTHFLYSSGDKQLRPSFLSSLSRSLTGARRLVETIFLGSRPW-----M 372
Db 485 SRSTVYPEKKFLYRSYQYFPKSFILSRLOQCAGGRLIETIFLSONPLKEQQNSL 544
QY 373 PGTPRRLPRLPQRYWQWRPLFLELLGNHACQPYGVLLKTHCP-----LRAA 418
Db 545 PQQWKRKRKLPRKYWQWREIFQKLKVHKECPYLFLRKNCVLLSACUKKTELTLQAA 604
QY 419 VTPAAGV-----CAREKPGQ-----SVAA-----PEE-----EDTDPRLRLVQLLRQ 454
Db 605 LPGEAKVHKHTEHGKSTEGTAPNSFLAPSPVLACQPERGEQHPAEGSDP-LLRELLRQ 663
QY 455 HSSPQWQYGFVRACLRRLVPPGLWGRHRRERFLRTKKFISLGKHAUKLSQBLTWMQSV 514
Db 664 HSSHQWQYGFVRECLERVIPAEALWSSHNKCRFFKNVKAFIGSKYAKLSLQQLMMKRV 723
QY 515 RDCAWLRRSPGVCVPAAEHRLREELIAKFLHMLMSVYVVELLRSFYVTTETFOKNRPF 574
Db 724 NDCVWLRLAKGNHVSFAYEHCYREELIAKFLYMLMSYVIELKSFYITETFOKNMLF 783
QY 575 FYRKSVMKLSQSIGIRQHLKRVOLRELSAEVQHREARPALTSRLRFPKPDGLRPV 634
Db 784 YRKFITWGLQNIQIRDFAKVHLRALSSSEMEVIRQKKVFPFASRLRFPKMWGLRPV 843
QY 635 NMDYVVGARTF---REEKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRWR 691
Db 844 RLRSRVVEGOKLSKESREKIQRYNTQKLFSLVNYERTVNTSIIGSSVFGRDDIYRKWK 903
QY 692 TFVLRV-RAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIAIIPK--QNTYCVRRVAVVQ 748
Db 904 EFYTKVFESGEMPHFYFVKGDVSRADTIPHKKLVEVISQVLKPSQTVYGRWAVIM 963
QY 749 KAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLOETSPLRDVAVIEOSSLSINASSGLFDV 808
Db 964 ITPTGKARKLYKRHVSTFEDFIPDMKQFVSKLQERTSLRNAIVVEOCLTFNENSTLFTF 1023
QY 809 FLREMFCHAVRJRGKSYVOCQIPGSGIILSTLLCSLCYGDMMENKLPAGIRRDGLLRLVD 868
Db 1024 FLQMLHNVLIEGHRYYIQCSGIPGSIILSTLLCSLCYGDMMENKLCGQKQGVLRLLD 1083
QY 869 DFLVTPHPLTHAKTFLRTLVRGVPYGVVNLKTVNPFVEDEALGTFVQMPAHGLF 928
Db 1084 DFLVTPHLMQARTFLRTIAAGIPYGVFLINAKTVNPFV-DDIPGCSKFHLPDCLJ 1142
QY 929 PNCGLLDTRTELEVSDSYSSYARTSIRASLTNRGFKAGNRMRKLVGVRLKCHSLFLD 988
Db 1143 SMCGLLDVQTLLEVYCDYSSAFTSIRSSLSFNSRIAGKNNCKLTAVLKLKCHPLLLD 1202
QY 989 LOVNSLQVCTNVIYKILLQAYRFHACVQLQLPFHQVWKNPFFFLRVISDTASLCYSILK 1048
Db 1203 LKINSLOTVLINIKYIFLLQAYRFHACVQLQFPNQVRNPDFFLRISDTASCCYFLK 1262
QY 1049 AKNAGMSLGAAGAAGPLPSEAVQWLCHOAFLLKLTTRHVVYVPLIGSLRTAQOLSRKLP 1108
Db 1263 AKNPGVSLGSKDASGMFFPEAAEWLCYHAFIVKLSNKHVYKCLLKPLKYVMHFLGKIP 1322
QY 1109 GTTLTALAAANPALPSPDKTILD 1132
Db 1323 RDTMELLKTVTEPSLCQDFKTILD 1346

RESULT 10

Q9DE32
ID Q9DE32 PRELIMINARY; PRT; 1191 AA.
AC Q9DE32;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name:TERT;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus.
RX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488334; PubMed=11602347;
RA Kuramoto M., Ohsumi K., Kishimoto T., Ishikawa F.;
RT "Identification and analysis of the Xenopus TERT gene that encodes the
RT catalytic subunit of telomerase.";
RL Gene 277:101-110(2001).
DR EMBL; AF212299; AAC73537.1; -;
DR CO; GO:0005634; C:nucleus; IEA.
DR CO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase.; IEA.
DR CO; GO:0016740; P:transferrase activity; IEA.
DR CO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RTase.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 2.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferrase.
SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match 38.9%; Score 2316.5; DB 2; Length 1191;
Best Local Similarity 42.4%; Pred. No. 4.9e-136;
Matches 518; Conservative 201; Mismatches 381; Indels 123; Gaps 25;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLG-PQGR--LVQRGDPAAPRALVAQCLVC 57
DB 1 MRLTGTGATLLSILORLYGVLGVEYDTLQVPGGKVPVLLLEGDSKFRSFVAELVVC 60

QY 58 VPWDARPPAAPSPQVSCLEKELVARVLQRCERGAKNVLAFLGALLDARGGPPPEAFTT 117
DB 61 IPRTCKPLPSPVFLQSTQREVVARVIQICEKKNVLAFLGGLVD-EKSNLIRLTP 119

QY 118 SVRSYLPNTVTDALRGSGALLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPLY- 176
DB 120 NICNYFNPPTTISTISILWETLLTRVGDDVMYWLQCSIFVFPVPRCCYQITGPIYT 179

QY 177 -----QLGANTQAR-----PPHASGPRRLGGERAWNHVRE 209
DB 180 LPSDVFLFQSQSTQSNVLLRYIKRVNHLRKKYLPKGSMTSRM-----LTWRRNKP 234

QY 210 AGVPLGLPAPGARRGGASRL-----PLPKRPRGAPE-----PERTPVGQG 254
DB 235 SGLLRKSTSMVATTEHSRKLCKSDICVDPKRRDNLKDXDTVDHFDLPMCRSYL 294

QY 255 SWAHPGR-----TRG-PSDRGFCVVSAPARAEATSLGALSGRH----- 294
DB 295 SNMYPKTNVQVTLITSGYKTKTFQCKPVCQKKTAPYSVAGDCNLSLKDNNKLI 354

QY 295 SHPSVGRQHAGPPSTGRPPWDTCPVVAETKFLY-SSGDKQLRSPFLSSLRPS 353
DB 355 TNASV-----PTAQR-----LSFSNIPIDFGRTLILYSIKYGFSEFSLNSLST 401

QY 354 LTGARRLVETIFLGS-----RPMVGTPLRPLPQRYWQMRPLFLLLGNHACPY 405
DB 402 PSGQKLVETIFLNFIAEQNDQKDENCY--KLPKRWKPKHFIQIHNKKFPY 459

QY 406 GVLLKTHCPURAAVTPAAGVCAREKPGQSVAAPEED-----TDPRLVLQLRQHS 457
DB 460 LVLYLNKHCPRVSS-----ACSEKR-----SLQKNRIENDGKQLKHTTKANLLSLKQHS 511

QY 458 PWQYGFVRACLRRLVPLGWSRHNRRFLRNTKFLISL-GKIAKLSLQBLTWMSVRD 516
DB 512 IWQYMFVRECLNNVDPIMWGSHNCRFRPNVKSFLFFSGKFGKISLSLWMSMRVD 571

QY 517 CAWLRRSPGVCVPAAEHRLREELTAKFLHLMVSVYVVELLSFFYVTTTFOKNRFFY 576
DB 572 CSWIRLQKSDHFVASEHLEKILAKFVFWMDTYVQLLKSFFYVTTTFOKNRFFY 631

QY 577 KSVWSKLQSIGIRQLKRVQLRELSBAEVRQHREARPALITSRLRIFPKDGLRPIVM 636

DB 632 RKSVWKQLQNGIRKHLKVKRLSLSSDELENMQQWKNVPLVSLRIFPKTNGLRPISKI 691
QY 637 DYVVGARTER--REKRAERLTSRVKALFVNLVYARRRPGLLGASVLGLDDIHAWRTFV 694
DB 692 SSTLSQSQSKENQEKIHHFSSQIRNLFVNLVYWRNCSLIGSVFGMDDIYKKNKXKV 751
QY 695 LRV-RAQDPPELIFYVKVDVTGAYDTIPQDRLTEVIAIIP--QNTYCVRRYAVVQKAA 751
DB 752 LDFEKPQVEKLQFVFKVTDVKGAYDTIPHSKLDVSVKVINPNANEVYCIIRYATVSDP 811
QY 752 HGVKRAFKSHVSTLTLQPYMQQFVAHLQETSPLRDAVVEIQSSSLNEASSGLFDVPLR 811
DB 812 TGRIRKSKFRHVBELADVLNPMKQFVSNQOEKLLRNTILVEQNLNLSVSKLLAVPQQ 871
QY 812 FMCHHVAIRIGKSVVQCQGIPOGSILSTLCSLCYGDWENKLPAGIRRDGLLRLLVDDFL 871
DB 872 IIRSHILIRIKORYMQCCGIPQGSMLSTILCSLCYGDWENAMLGGIQXGVLMRLDIDL 931
QY 872 LVTPHLTHAKTFLRLTVRGVPEYGCVVNLKRTVVNPFVED--EALGGTAFVQMPAHGLFP 929
DB 932 LVTPHLQAKTFLRLTLAGIPQYGCISIPQKTVVNFVDDIPEC---SEVEQLPSHCLFR 988
QY 930 WCGLLDTRLEVSQDYSSYARTSIRASLTFRNGFKAGRNMRKLFGLVRLKCHSLFDL 989
DB 989 WCGLLDTQTLVDYDYSSYACTSIRSSMTFCHSSAAGKYMQLIRVLRKCHSLFDL 1048
QY 990 QVNSLQVTCNIVKILLQAVRPHACVLQLPFHQOVWKNPTFFLVRVSDTASLCVSLKA 1049
DB 1049 KVASLRTVCINTYKIFLQAIRHACVVQPFQGVQVNNPFFLTVISDMAPCYFTTFA 1108
QY 1050 KNAGMSLGAKGAAGPLSEAVQMLCHQAFLLKLTTRHRTVTVPLVGLSLRTAQLSRKLP 1109
DB 1109 KNKDLTRGYKDVSCQNFQVAVQMLSYQAFLLKLNHVKLYKCLIGPLQNCQKQLSRRLSQ 1168
QY 1110 TTTTALAAANPALPSDFKTLID 1132
DB 1169 DTIELLSKSVTSSLLHKDFSCIMD 1191

RESULT 11
O94807 PRELIMINARY; PRT; 523 AA.
AC O94807;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Telomerase transcriptase (fragment).
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99137484; PubMed=9973199;
RA Takakura M., Kyo S., Kanaya T., Hirano H., Takeda J., Yutsudo M.,
RA Inoue M.;
RT "Cloning of human telomerase catalytic subunit (hTERT) gene promoter
RT and identification of proximal core promoter sequences essential for
RT transcriptional activation in immortalized and cancer cells.";
RL Cancer Res. 59:551-557(1999).
DR EMBL; AB016767; BAA74724.1;
FT NON TER 523 523
SQ SEQUENCE 523 AA; 56555 MW; 8FDE562DDECC93DA CRC64;

Query Match 37.0%; Score 2207.5; DB 2; Length 523;
Best Local Similarity 78.7%; Pred. No. 1.1e-129;
Matches 435; Conservative 3; Mismatches 56; Indels 59; Gaps 6;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPRALVAQCLVCVPW 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPRALVAQCLVCVPW 60

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QY 61 DARPPPAAPSFQVSCIKELVARVLQRCERGAKNVLAFLDGDGARGGPPFAFTTSVR 120
DB 61 DARPPPAAPSFQVSCIKELVARVLQRCERGAKNVLAFLDGDGARGGPPFAFTTSVR 120
QY 121 SYLPTNTVDALRSGGALLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVDALRSGGALLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGLPAPGARRGGSSASLSLPKPRR 240
DB 181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGLPAPGARRGGSSASLSLPKPRR 240
QY 241 GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300
QY 301 ROHAGAPSTSRPPRWDTPCPVYATKHIFLYSSGDKQOLRPSFLSSLRPLTGARRL 360
DB 301 ROHAGAPSTSRPPRWDTPCPVYATKHIFLYSSGDKQOLRPSFLSSLRPLTGARRL 360
QY 361 VETIFLGSRPMPCTPRRLPRLQRYWQMRPLFLELLGNHAQCPYGVLLKXTHCPLRAVT 420
DB 361 VETIFLGSRPMPCTPRRLPRLQRYWQMRPLFLELLGNHAQCPYGVLLKXTHCPLRAVT 420
QY 421 PAAGVCAREKPGQSWAAPBEEDTDPRRLVQLLRQHSSPQVYGFVRACLRRLVPPGLW-- 478
DB 421 PAAGVCAREKPGQSWAAPBEEDTDPRRLVQLLRQHSSPQVYGFVRACLRRLVPPGLW-- 478
QY 479 -----GSRHNRRLRNTKFTISLGKHAQLSLQELTWK 511
DB 479 -----GSRHNRRLRNTKFTISLGKHAQLSLQELTWK 511
QY 512 MSVRDCAWLRRSP 524
DB 512 MSVRDCAWLRRSP 524
QY 511 MSVRDCAWLRRSP 523
DB 511 MSVRDCAWLRRSP 523
RESULT 12
Q9JK99 PRELIMINARY; PRT; 575 AA.
AC Q9JK99;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DE Telomerase catalytic subunit (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=22860253; PubMed=13679242;
RA Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RT "Cloning of rat telomerase catalytic subunit functional domains,
RT reconstitution of telomerase activity and enzymatic profile of pig and
RT chicken tissues.";
RL Life Sci. 73:2749-2760(2003).
RN [2]
SEQUENCE FROM N.A.
RP Wong S., Gao S., Xu X., Yu H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF247818; AAF62177.1; -.
CO; GO:0005634; C:nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR GO:0003964; F:telomeric template DNA polymerase activity; IEA.
DR GO:0003721; F:telomeric template RNA reverse transcriptase; IEA.
DR GO:0016740; P:transference activity; IEA.
DR GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR004047; RVTSE.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
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DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
Query Match 33.8%; Score 2016; DB 2; Length 575;
Best Local Similarity 67.6%; Pred. No. 1.2e-117;
Matches 391; Conservative 71; Mismatches 110; Indels 6; Gaps 3;
QY 558 RSFFYVTEFTQKRLFFYRKSVMSKLSQSTIGIHOHLKRVOLRELSEAEVQREARALL 617
DB 1 RSFFYVTEFTQKRLFFYRKSVMSKLSQSTIGIHOHLKRVOLRELSEAEVQREARALL 617
QY 618 TSRLRPIKPDGLRPIVNNDDYVVGARTFRREKAEALRTSRVKALFSLVNYERARRPGLLG 677
DB 61 ICLRLRIPENGLRPIVNNDDYVVGARTFRREKAEALRTSRVKALFSLVNYERARRPGLLG 677
QY 678 ASVLGLDDIHRARWTRFVLVRADPPPELYFVKVDTGAYDTTIPQRLTEVIAIHK-PQ 736
DB 121 SSVLGMNDIYRTWRAFLVRALDQTPRMVFKADVTGAYDAIPQGLVVEVAMIRHSE 180
QY 737 NTVCYRYAVVQKAAHGHYRKAFKSHVSTLTDLQPYMRQFVAHLQET--SPLSDAVVIEQ 794
DB 181 STYCIHQYAVVRDSQGVHKSFRQVTTLSDLQPYMRQFVAHLQET--SPLSDAVVIEQ 794
QY 795 SSSLSNEASSGLFDVFLRFMCHHAVIRGRKSVYVQCGIPQGSILSTLLCSLCYGDMMENKLF 854
DB 241 STSMNESSSLDFLHLFRLHRSVVKIGDRCTYQCGIPQGSILSTLLCSLCYGDMMENKLF 854
QY 855 AGIRRDGLLLRLVDDFLVTPPHLTHAKTFLRLTVRGVPEYGCVVNLKRTVNVFPVEDEAL 914
DB 301 AEVQRDGLLLRFVDDFLVTPPHLTHAKTFLRLTVRGVPEYGCVVNLKRTVNVFPVEDEAL 914
QY 915 GGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSSYARTSIRASLTNRGFKAGNRKRL 974
DB 361 GGAAPYQLPAHCLFPWCGLLDTRTLEVSQSDYSSYARTSIRASLTNRGFKAGNRKRL 974
QY 975 FGVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQFPHQOVKNPTFFLR 1034
DB 421 LSVRLKCHGLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQFPHQOVKNPTFFLR 1034
QY 1035 VISDTASLCYSILKAKNAGMSLGAAGAAGPLPSEAVQWLCHQAFLLKLTRHRYVYVPLLG 1094
DB 481 IISQASCCVAILKVNKPGWTLKASG---FPPEAAHWCYQAFLLKLAHSAHVIYKCLLG 537
QY 1095 SURTAQTLQSRKLPGLTTLTALEAANPALPSDEKTLID 1132
DB 538 PURTAQTLQSRKLPGLTTLTALEAANPALPSDEKTLID 575
RESULT 13
Q9R266 PRELIMINARY; PRT; 514 AA.
AC Q9R266;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN Name=tert;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=99144726; PubMed=10022128;
RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R.,
RA Lichtsteiner S., Chin L., Morin G.B., Depinho R.A.;
RT "Telomerase reverse transcriptase gene is a direct target of c-Myc but
RT is not functionally equivalent in cellular transformation.";
RL Oncogene 18:1219-1226(1999)
DR EMBL; AF121949; AAD24465.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
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DR	GO:0003677; F:DNA binding; IEA.	DR	GO:0003677; F:DNA binding; IEA.
DR	GO:0003723; F:RNA binding; IEA.	DR	GO:0003723; F:RNA binding; IEA.
DR	GO:0003964; F:RNA-directed DNA polymerase activity; IEA.	DR	GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR	GO:0003721; F:telomeric template RNA reverse transcriptase. . . ; IEA.	DR	GO:0003721; F:telomeric template RNA reverse transcriptase. . . ; IEA.
DR	GO:0015740; F:transferase activity; IEA.	DR	GO:0015740; F:transferase activity; IEA.
DR	GO:0006276; F:RNA-dependent DNA replication; IEA.	DR	GO:0006276; F:RNA-dependent DNA replication; IEA.
DR	InterPro: IPR000215; Prot_inh_serpin.	DR	InterPro: IPR000215; Prot_inh_serpin.
DR	InterPro: IPR000477; RVTse.	DR	InterPro: IPR000477; RVTse.
DR	Pfam: PF00078; RVT; 1.	DR	Pfam: PF00078; RVT; 1.
DR	PRINTS: PR01365; TELOMERASERT.	DR	PRINTS: PR01365; TELOMERASERT.
DR	PROSITE: PS00284; SERPIN; UNKNOWN 1.	DR	PROSITE: PS00284; SERPIN; UNKNOWN 1.
KW	RNA-directed DNA polymerase; Transferase.	KW	RNA-directed DNA polymerase; Transferase.
SQ	SEQUENCE 1123 AA; 130551 MW; 44248295817B7F6 CRC64;	SQ	SEQUENCE 1123 AA; 130551 MW; 44248295817B7F6 CRC64;
Query Match 12.2%; Score 724.5; DB 2; Length 1123;			
Best Local Similarity 23.9%; Pred. No. 1.6e-36;			
Matches 294; Conservative 192; Mismatches 506; Indels 237; Gaps 39;			
QY	1 MPRAPRCRAVRSLLRSHYREVLPLATFV-----RRLGPGQWR-----L 38	QY	1 MPRAPRCRAVRSLLRSHYREVLPLATFV-----RRLGPGQWR-----L 38
Db	1 MPKPRHRVPEILLMRLFGNRRARNLDAIVDLIPNRNIQPEQCRGOGCLGCSDDKPAFL 60	Db	1 MPKPRHRVPEILLMRLFGNRRARNLDAIVDLIPNRNIQPEQCRGOGCLGCSDDKPAFL 60
QY	39 VORGDDPAFRAVAQCLVCVPWDARPPPAAPSPFQVSKLKBELVARVLQRL---CERGAKN 95	QY	39 VORGDDPAFRAVAQCLVCVPWDARPPPAAPSPFQVSKLKBELVARVLQRL---CERGAKN 95
Db	61 LRSDDDPIHYRKLHRCFV-VLHEQTPLLDPSPSWMNSQREIVERIETEMQSGCD--CQN 117	Db	61 LRSDDDPIHYRKLHRCFV-VLHEQTPLLDPSPSWMNSQREIVERIETEMQSGCD--CQN 117
QY	96 VLAFCFALLDARGCGPPBEAFTTSVRSVLPNTVTDALRSGAGWGLLRVGDVVLHLLAR 155	QY	96 VLAFCFALLDARGCGPPBEAFTTSVRSVLPNTVTDALRSGAGWGLLRVGDVVLHLLAR 155
Db	118 VICARYDKDOS-----SPILBLT-SSWEFLLKRVGHVNVVYLQQ 159	Db	118 VICARYDKDOS-----SPILBLT-SSWEFLLKRVGHVNVVYLQQ 159
QY	156 CALFVLVAPSCAYQVCGPPLYQLGAAT-----QARPPPHASGRRLRGGERAWNHSVRE 209	QY	156 CALFVLVAPSCAYQVCGPPLYQLGAAT-----QARPPPHASGRRLRGGERAWNHSVRE 209
Db	160 TSIFLPLGKXHQVSGPPLCIKHKRTLSVHNKRKDDNVQPTKQWLSSAVDDCPKD 219	Db	160 TSIFLPLGKXHQVSGPPLCIKHKRTLSVHNKRKDDNVQPTKQWLSSAVDDCPKD 219
QY	210 AGVPLGLPAG-----ARRGGSASRSPLPKRPRRGA-----APEPRTVPGQSGWA 257	QY	210 AGVPLGLPAG-----ARRGGSASRSPLPKRPRRGA-----APEPRTVPGQSGWA 257
Db	220 DSATI-TPIVGEDVDQHREKTKTTRSRILYLRKREKQKRVFKVDCNAPCITP----- 271	Db	220 DSATI-TPIVGEDVDQHREKTKTTRSRILYLRKREKQKRVFKVDCNAPCITP----- 271
QY	258 HPGRTGRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVGRQHHAGPPSTSRPPRW 317	QY	258 HPGRTGRGSDRGFCVSPARPAEATSILEGALSGTRHSHPSVGRQHHAGPPSTSRPPRW 317
Db	272 ---STNGKVSTG-----NDENMLHIGINGSLTDFVKAQKQ----- 303	Db	272 ---STNGKVSTG-----NDENMLHIGINGSLTDFVKAQKQ----- 303
QY	318 DTPCCPVYAETKHFLYS--SGDKEQLRPSFLISSRLPSLITGARRLIVETIFLGRSPWMPGTP 376	QY	318 DTPCCPVYAETKHFLYS--SGDKEQLRPSFLISSRLPSLITGARRLIVETIFLGRSPWMPGTP 376
Db	304 -----VKNKNFKGLSEYTSVIPPNNHILKTLRPNCSDSKULMNHIFGEVNVVSTTPS 356	Db	304 -----VKNKNFKGLSEYTSVIPPNNHILKTLRPNCSDSKULMNHIFGEVNVVSTTPS 356
QY	377 RRLPLPQ-----RYQWRPLFLELLGNHAQCYPVGLKTHCP-----LRAAVTPAAG 424	QY	377 RRLPLPQ-----RYQWRPLFLELLGNHAQCYPVGLKTHCP-----LRAAVTPAAG 424
Db	357 HGKGNCPSGSICLYHSLLSKLNIGTKTSSHLKMLLDKHCPLVLLQEDALKSGTTSQSS 416	Db	357 HGKGNCPSGSICLYHSLLSKLNIGTKTSSHLKMLLDKHCPLVLLQEDALKSGTTSQSS 416
QY	425 VCAREK-----PQGSVAA-----PEBEDTDPRLVQLLQHSPPQVYFVACLRLLVPPG 476	QY	425 VCAREK-----PQGSVAA-----PEBEDTDPRLVQLLQHSPPQVYFVACLRLLVPPG 476
Db	417 --RRQADKLPHGSSSSQTKPKCPSVEERKL-----YCTNDQVVSFIWAI CRYIIVPES 468	Db	417 --RRQADKLPHGSSSSQTKPKCPSVEERKL-----YCTNDQVVSFIWAI CRYIIVPES 468
QY	477 LMGSRHNRRLRNTKKPFISLGKAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEAHRL 536	QY	477 LMGSRHNRRLRNTKKPFISLGKAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEAHRL 536
Db	469 LLGTHQWRVLRKNIAMFVSRNRNEKCTVQVFLHKVPSPDFPFARKE--LCCMWNGHEL 526	Db	469 LLGTHQWRVLRKNIAMFVSRNRNEKCTVQVFLHKVPSPDFPFARKE--LCCMWNGHEL 526
QY	537 REE-----ILAKFLHMLMSVVVBLRLSFFVYTTTTFQKNRLFPYRKSVMSKLSQISG 588	QY	537 REE-----ILAKFLHMLMSVVVBLRLSFFVYTTTTFQKNRLFPYRKSVMSKLSQISG 588
Db	527 QSESIRSTQQMLCTKWISWLFLEIVKLVHFNFPYATSGOGLRNIIYYRKRSWERLISKE 586	Db	527 QSESIRSTQQMLCTKWISWLFLEIVKLVHFNFPYATSGOGLRNIIYYRKRSWERLISKE 586
QY	589 IROHLKRVOLRELSAEVRQHREARPAALLTSRLRFPFKPDGLRPIVMDVYVGARTFRRE 648	QY	589 IROHLKRVOLRELSAEVRQHREARPAALLTSRLRFPFKPDGLRPIVMDVYVGARTFRRE 648
Db	587 ISKALDGVYLVDDAEASSRKK-----LSKFRFLKANGVRMLD-----FSSS 630	Db	587 ISKALDGVYLVDDAEASSRKK-----LSKFRFLKANGVRMLD-----FSSS 630
QY	649 KRAERLTSRVKALPSVLNRYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPP--PELY 707	QY	649 KRAERLTSRVKALPSVLNRYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPP--PELY 707
Db	631 SRSQSL-----RDTHAVLKDQLKEPDVILGSSVFDHDDFYRNLCFYLHLRSQSGELPPLY 686	Db	631 SRSQSL-----RDTHAVLKDQLKEPDVILGSSVFDHDDFYRNLCFYLHLRSQSGELPPLY 686
QY	708 FVKVDVTGAYDTIPQDRLITEVIASIIKPNQTYCVRRYAVVOKAAHGH-----VRKAFKS 761	QY	708 FVKVDVTGAYDTIPQDRLITEVIASIIKPNQTYCVRRYAVVOKAAHGH-----VRKAFKS 761

Db 687 FVADVFPKAPSDVDQKLLHVIOSFLKDE--YILNRCRLVCCGKRSNNWNKILVSSDKNS 744
QY 762 HVSTLTDLQPMRQFVAHQLETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVRIR 821
Db 745 NFRFTSTVPINA-----LQ-----SIVVDGENHRVRKKDLMVMWGNLKNMLQLD 792
QY 822 GKSYVQCGIPQGSIIITLCSLCYGDMEKLFAGI-----RRDGL----- 862
Db 793 KSFFVQIAGIPQGHRLSSLLCCFYGHLERTLIVPFLFEASKDVSSKECSREBELIPTS 852
QY 863 --LLRLVDDFLVTPHAKTFLRTLVRGPEYGCVVNLRKTVNPPVEDE----- 912
Db 853 YKLLRFDDDLVFTSRDQASSFVRLKHGFKDYNCFMNETKFCINPDKEDKEHRCSNRM 912
QY 913 --ALGGTAFVQMPAHGLFPNCGLLDRTLLEVQSDYSSYARTSIRASLTENRFGKAGNM 970
Db 913 FVGDNVPPFVR-----WTGLINSRTFEVQVDYTRYLSGHISSTFSVAMQNKVPRNL 964
QY 971 RRLFGVRLRLKHSFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFFHQVWK-NP 1029
Db 965 RQKLCYELVPKCHPILPDSNINGSIEVRLNIYQIFLLAAMKFCYVVEV---SRFWKLHP 1021
QY 1030 TFLRVISDTASLCYSILKNAKMSLGAK-GAAGPLPSEAVOMLCHQAPLLKLTNRHVT 1088
Db 1022 QTLFKFTISVRYMFRLINRRVRRINTGSSFRPVLKLYKEEVWLGLDAYIQVLKKNRS 1081
QY 1089 YVPLGSLRTA-----QTOLSRKLPQTT 1111
Db 1082 YRMLLIYLSKLSKLSQSLSELKYAT 1110

RESULT 15
Q9SPU7 PRELIMINARY; PRT; 1123 AA.
AC Q9SPU7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Telomerase reverse transcriptase.
GN Name=ATERT; Synonyms=FSE19_190;
OS Arabidopsis thaliana (Mouset-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99402974; PubMed=10471830;
RA Oguchi K., Liu H., Tamura K., Takahashi H.;
RT "Molecular cloning and characterization of AtTERT, a telomerase
reverse transcriptase homolog in Arabidopsis thaliana.";
RL FEBS Lett. 457:465-469 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN EMBL; AF135454; AAD54777.1; -;
DR EMBL; AL391147; CAC01849.1; -;
DR PIR; T51517; T51517.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR InterPro; IPR000477; RVTse.

DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS00284; SERPIN; UNKNOWN 1.
KW RNA-directed DNA polymerase; transferase.
SQ SEQUENCE 1123 AA; 130579 MW; 5645B8295817B7F6 CRC64;

Query Match 12.2%; Score 724.5; DB 2; Length 1123;
Best Local Similarity 23.8%; Pred. No. 1.6e-36;
Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;

QY 1 MPRAPCRRAVRSLRSHREVLPPLATFV-----RRLPGQWR-----L 38
Db 1 MPKPKRHRVPEILWLFLGNRARNLNDIAIVDLIPNRNIQPCRCRGQGLGSSDKPAFL 60
QY 39 VORGDPAAFRALVAQCLVCPWDARPPPAAPSPFRQVSCLELVARVQLRL---CERGAKN 95
Db 61 LRSDDPIHYRKLHLRCFV-VLHEQTPPLDLDFTSNWSOREIVERIEMMQSGCD--CON 117
QY 96 VLAFGFALLDGAAGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGDVVLHLLAR 155
Db 118 VICARYDKYDQS-----SPLELLT-SSSWEFLKRVGHVDMVYLLQ 159
QY 156 CALFVLVAPSCAYQCGPPLXQLGAAT-----QARPPHAPGRRRLCGERAMNHSVR 209
Db 160 TSIFLPLGLGKHQVSGPPLCIKHKRTLSVHENKRRDDNVQPTKRWLSSAVDDCPKD 219
QY 210 AGVPLGLPAPG---ARRGGASRSLPLPKPRGA-----APEPERTVPGQSWA 257
Db 220 DSATI-TPIVGEDVDQHREKTKTSRIYLRKRRKQKYNFKKVDCAFCITP----- 271
QY 258 HPGRTGPGSDRGFCVVSPARPAEATSLGALSQTRHSHPSVGRQHGAGPPSTRPRPW 317
Db 272 ---STNGKVSTG-----NDENLHIGINGSLTDFVKQAKQ----- 303
QY 318 DTPCPPVYAEATKFLYS-SGDKEQLRPSFLLSLRSLTGARRLVETIFLGRPMMPGT 376
Db 304 -----VKNKNFKFGLSETYSVTPPNHILKTLRPNCSKLLMNHIFGEVNVWSTPS 356
QY 377 RRLPLRPQ---RYWQMRPLFLELGNHAQCPYVLLKTHCP-----LRAAVTPAG 424
Db 357 HGKGNCPGSGICLYHSLKSLKXNLGKTKSSHLKMLLDKHPVLLQEDALSGTTSQS 416
QY 425 VCAREK----PGGSVAA----PEEEDTPRLVQLLRQHSHPQVYGFVACLRRLRVP 476
Db 417 --RRQADKLPHGSSSGTGKPKCSVERKL-----YCTNDQVVSFWAICRYIVPS 468
QY 477 LMGSRHNRRLNTKCFISLQGHAKLSQELTWKMSVRDCAWLRRSPGVCVPAAEHL 536
Db 469 LLGTTQMRVLRKNIAWFVSRRRNEKCTVQFLHKVKPSDFPFARKE--LCCMVNGHEL 526
QY 537 REE-----ILAFELHWMVYVVELLRSFPYVTEFTFQKNRLLFFYKSVMSKLQSIG 588
Db 527 QSESIHQMLCTKWISWLFLEIVKLVHFNFYATESQGGRLNIYYIKRSMERLISKE 586
QY 589 IRQHLKRVOLRELSAEVROHREARPALUTSLRFLPKDPGLRPIVMYVVGARFRRE 648
Db 587 ISKALDGYLVDDAEASRKK-----LSRFLPKANGVRWLD-----FSSS 630
QY 649 KRAERLTSRKALFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVADQPP-PELY 707
Db 631 SRQSGL---RDTHAVLKDIQLKEPDLGSSVDFDHFYRNLCPLYLHLSRQSGLPPLY 686
QY 708 FVKVDVTGAYDTIPQDRLTEVIASIKPQNTYCVRYAVVQKAACH-----VRKAFKS 761
Db 687 FVADVFKAFDSVDQKLLHVIQSFLKDE--YILNRCRLVCCGKRSNNWNKILVSSDKNS 744
QY 762 HVSTLTDLQPMRQFVAHQLETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVRIR 821
Db 745 NFRFTSTVPINA-----LQ-----SIVVDGENHRVRKKDLMVMWGNLKNMLQLD 792
QY 822 GKSYVQCGIPQGSIIITLCSLCYGDMEKLFAGI-----RRDGL----- 862

Db	793	KSFYVQIAGIPQGHRLSSLLCCFYVYGHLERTLIIYPFLEEASKOVSSKECSREBELIIPTS	852
Qy	863	--LLRLVDDFLLTPTPHLTHAKTFLRTLVRGVPYGCYVNLKRTVVNFPFVEDE-----	912
Db	853	YKLLRFDDYLFVTSRDQASSFYHRLKHGFKDYNCFMNETKFCINFEDKEEHRCSSNRM	912
Qy	913	--ALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSYARTSTRASLTFRNGFKAGRNM	970
Db	913	FVGDNQVPFVR-----WTGLLINSRTFEVQVDYTRYLSGHISSSTFSVAWQNKPVRL	964
Qy	971	RRKLPGLRLKCHSLFLDLQVNSLQTVCTNLYKILLQAYRFHACVLQLPHEHQOVWK-NP	1029
Db	965	RQKLCYFLVPKCHPILFDSNINSGEIVRLNIYQIFLLAAMKFCYVYEV---SRFWKLHP	1021
Qy	1030	TFFLRVISDTASLCYSILKAKNAGMSLGAK-GAAGPLPSEAVOWLCHQAFLLKLTRHRVT	1088
Db	1022	QTLFKFITISVRVWFLNRVRINTGSSFRPVLYKEEVIWGLDQVYIQLVKKNSR	1081
Qy	1089	YVPLLSLRTAQTO--LSRKLPGTTLTALEAAAPAL	1123
Db	1082	YRMLLIYKLSALSKHLSQLSSELRYATDRSNSSSL	1118

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Job time : 222 secs

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-851-843A-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRLRPGQWRLVQGDPAAPRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRLRPGQWRLVQGDPAAPRALVAQCLVCVPW 60

Qy 61 DARPPAPRSPROVSCIKELVARVLQRLCERGAQNVLAFGFALLDARGGPPPEAFTSVR 120
Db 61 DARPPAPRSPROVSCIKELVARVLQRLCERGAQNVLAFGFALLDARGGPPPEAFTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLVOLGA 180

Qy 181 ATQARPPHAGSPRRRLGCRANWHSVREAGVPLGLPAPGARRRGGASRSLPLPKRPR 240
Db 181 ATQARPPHAGSPRRRLGCRANWHSVREAGVPLGLPAPGARRRGGASRSLPLPKRPR 240

Qy 241 GAAPERTPVGGSWAHPCGTRGSDRGFCVVSPPARPAEATSLGALSGTTHSHPSVG 300
Db 241 GAAPERTPVGGSWAHPCGTRGSDRGFCVVSPPARPAEATSLGALSGTTHSHPSVG 300

Qy 301 RQHAGPPSTSRPPMDTPCPVYAEKHFLLYSSGDKQOLRPSFLLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPMDTPCPVYAEKHFLLYSSGDKQOLRPSFLLSSLRPSLTGARRL 360

Qy 361 VETIFGSRPWPMTGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFGSRPWPMTGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy 421 PAAGVCAREPQGSVAAPESDTPRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWS 480
Db 421 PAAGVCAREPQGSVAAPESDTPRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWS 480

Qy 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAABHRLREEI 540
Db 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAABHRLREEI 540

Qy 541 LAKPLHLMMSVYVVELLRSPFYVTETTFQKRLFFYRKSVWSKLQSIGIRQHLKRVOLRE 600
Db 541 LAKPLHLMMSVYVVELLRSPFYVTETTFQKRLFFYRKSVWSKLQSIGIRQHLKRVOLRE 600

Qy 601 LSAEVRQHREARPAALLTSRLREIPKPDGLRPIVNDYVVGARTFRREKRAELTSRVKA 660
Db 601 LSAEVRQHREARPAALLTSRLREIPKPDGLRPIVNDYVVGARTFRREKRAELTSRVKA 660

Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTEFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTEFVLVRAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PQRLTEVIASITKPNQTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PQRLTEVIASITKPNQTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780

Qy 781 QETSPLRDVAVVIQSSSLNEASGLFDVFLRFCHHAVRIRGKSVYQCOGIPGGSITLSTL 840
Db 781 QETSPLRDVAVVIQSSSLNEASGLFDVFLRFCHHAVRIRGKSVYQCOGIPGGSITLSTL 840

Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDPFLVTPHLTHAKTFLRTLVRGPYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDPFLVTPHLTHAKTFLRTLVRGPYGCVVNL 900

Qy 901 RKTVMNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSYVARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSYVARTSIRASLTF 960

; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harlev, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-549A-2

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPRAPRCRAVRSLLRSYREVLPLATFVRRLLGPGQWRLVQRGDDPAAFRALVAQCLVCPW	60
Db	1	MPRAPRCRAVRSLLRSYREVLPLATFVRRLLGPGQWRLVQRGDDPAAFRALVAQCLVCPW	60
Qy	61	DAREPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPPPEAFTTSVR	120
Db	61	DAREPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPPPEAFTTSVR	120
Qy	121	SYLNTVTVDALRGSGANGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVGGPPLYOLGA	180
Db	121	SYLNTVTVDALRGSGANGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVGGPPLYOLGA	180
Qy	181	ATOARPPHAGSPRRRLGCRANWHSYREAGVPLGLPAGBARRGSGASRLPLPKPRR	240
Db	181	ATOARPPHAGSPRRRLGCRANWHSYREAGVPLGLPAGBARRGSGASRLPLPKPRR	240
Qy	241	GAAPERTPVQGSWAHPGRTGSPDRGFCVSPAPAEATSLGALSGTRHSHPSVG	300
Db	241	GAAPERTPVQGSWAHPGRTGSPDRGFCVSPAPAEATSLGALSGTRHSHPSVG	300
Qy	301	RQHAGPPTSRPRPMDTCPVYAEKHFVLYSSGDKQLRPSFLSSRLSPSTGARRL	360
Db	301	RQHAGPPTSRPRPMDTCPVYAEKHFVLYSSGDKQLRPSFLSSRLSPSTGARRL	360
Qy	361	VETIFLGSRPMPCTPRRLPLPORYWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT	420
Db	361	VETIFLGSRPMPCTPRRLPLPORYWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT	420
Qy	421	PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSFPWQYGFVRACLRLVPPGLWGS	480
Db	421	PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSFPWQYGFVRACLRLVPPGLWGS	480
Qy	481	RHNERRFLRNTKFIISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCPVAAEHLREEI	540
Db	481	RHNERRFLRNTKFIISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCPVAAEHLREEI	540
Qy	541	LAKELHLMMSVYVVELLRSFPYVTTTFQKNRLFFYKSWSKLQSIGIROLKRVOLRE	600
Db	541	LAKELHLMMSVYVVELLRSFPYVTTTFQKNRLFFYKSWSKLQSIGIROLKRVOLRE	600
Qy	601	LSEAEVQHREARPAALLTSRLRFTPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA	660
Db	601	LSEAEVQHREARPAALLTSRLRFTPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA	660
Qy	661	LFSVLNYERARRPGLGASVGLGDDIHRAMWTFVLRVRAQDDPPPELYFVKVDVTGAYDTI	720
Db	661	LFSVLNYERARRPGLGASVGLGDDIHRAMWTFVLRVRAQDDPPPELYFVKVDVTGAYDTI	720
Qy	721	PODLRTEVIAIIIPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLQPYMQFVAHL	780
Db	721	PODLRTEVIAIIIPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLQPYMQFVAHL	780

Qy	781	QETSPURDAVVIEQSSSLNEASSGLFDVFLRFMCHHVAIRIRGKSYVOCQIPQGSILSTL	840
Db	781	QETSPURDAVVIEQSSSLNEASSGLFDVFLRFMCHHVAIRIRGKSYVOCQIPQGSILSTL	840
Qy	841	LCSLCYGDMENKLFAGIRRDGLLRLLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900
Db	841	LCSLCYGDMENKLFAGIRRDGLLRLLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900
Qy	901	RKTVMFPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVOQSDYSYARTSIRASLTF	960
Db	901	RKTVMFPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVOQSDYSYARTSIRASLTF	960
Qy	961	NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP	1020
Db	961	NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP	1020
Qy	1021	FHOQVKNPPTFFLRVISTDASLCYSILKAKNAGNSILGAKAAGPLPSEAQVWLCHQAFLL	1080
Db	1021	FHOQVKNPPTFFLRVISTDASLCYSILKAKNAGNSILGAKAAGPLPSEAQVWLCHQAFLL	1080
Qy	1081	KLTRHRVTVYVPLLGSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD	1132
Db	1081	KLTRHRVTVYVPLLGSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD	1132

RESULT 3
US-08-854-050-225
; Sequence 225, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

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;
;
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-854-050-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSYHREVLPLATFVRLRGPGWRLVORGDPAAFRALVAQCVCVPW 60
Db 1 MPAPRCRAVRSLLRSYHREVLPLATFVRLRGPGWRLVORGDPAAFRALVAQCVCVPW 60
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Db 61 DARPPPAAPSROYSCLEKELVARVLRQRCERGAKNVLAFGALLDGGAGGPPFAFTSVR 120
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Db 121 SYLPTNTVDALRGSGANGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
QY 181 ATQARPPHAGPPRRRLGCRAMNHSVREAGVPLGLPAGARRGGSGASRLPLPKRPRR 240
Db 181 ATQARPPHAGPPRRRLGCRAMNHSVREAGVPLGLPAGARRGGSGASRLPLPKRPRR 240
QY 241 GAAPEPERTVPGQGSWAHPGRTGSPDRGFCVVSPPAPAEATSLEGALSGTRHSPSVG 300
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QY 301 RQHAGPPSTSRPPRPWDTPCPVYAEKHFLLSYSSGDKQLRPSFLLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPRPWDTPCPVYAEKHFLLSYSSGDKQLRPSFLLSSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRRLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRRLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREPQGSVAAPPEEDTDPRRLVOLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREPQGSVAAPPEEDTDPRRLVOLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERRLRNTKXKFI SLGKHAKLSQLBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRLRNTKXKFI SLGKHAKLSQLBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
QY 541 LAKFLHLMVSVYVELLSRFYFYTETTFQKNRLFFYRKSVWSKLQSIGIRQHHLKRVOLRE 600
Db 541 LAKFLHLMVSVYVELLSRFYFYTETTFQKNRLFFYRKSVWSKLQSIGIRQHHLKRVOLRE 600
QY 601 LSAEVRQHREARPAALLTSRLRIPKPDGLRPIVNDYVVGARTFRREKRAELTSRVKA 660
Db 601 LSAEVRQHREARPAALLTSRLRIPKPDGLRPIVNDYVVGARTFRREKRAELTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLREVTASIIKPQNTYCVRYAYVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PQDLREVTASIIKPQNTYCVRYAYVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIQSGSLSTL 840
Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIQSGSLSTL 840

841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYVARTSIRASLTF 960
901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYVARTSIRASLTF 960
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1021 FHOQVWKNPTFFLRVTSIDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
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1081 KLTRHRVTVPVLLGSLRTAQTLQSRKLPCTTTLTAAEAAANPALPSDFKTILD 1132
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RESULT 4
US-09-430-323-225
; Sequence 225, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lirgner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Towneend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-09-430-323-225

Query Match      100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQRGDDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQRGDDPAAFRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSPROVSCSKELVARVLQRLCERGAKNVLAFGFPALLDGGARGGPEAFTTSVR 120
Db 61 DARPPPAAPSPROVSCSKELVARVLQRLCERGAKNVLAFGFPALLDGGARGGPEAFTTSVR 120

Qy 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
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Qy 181 ATQARPPHAGSPRRRLGCCRANVHNSVREAGVPLGLPAPGARRRGGSGASRSLPLPKPRR 240
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Qy 241 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300

Qy 301 RQHAGPPSTSRPRPDWTPCPVYAEKHFLLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPRPDWTPCPVYAEKHFLLYSSGDKQELRPSFLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRPWPGTTPRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWPGTTPRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy 421 PAAGVCAREKPGQSAVAPEEEDTDPRLVQLLRQHSFPWQYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSAVAPEEEDTDPRLVQLLRQHSFPWQYGFVRACLRRLVPPGLWGS 480

Qy 481 RHNERRFLNNTKFIISLGKHAKLSLOELTWKMSVDCNWLRRSPGVCVCPAAEHLRLEE 540
Db 481 RHNERRFLNNTKFIISLGKHAKLSLOELTWKMSVDCNWLRRSPGVCVCPAAEHLRLEE 540

Qy 541 LAKFLHLMMSYVVVELLRSFFVTETTFQKNRLFYRKSVMSKLSQIGIROHLKRVOLRE 600
Db 541 LAKFLHLMMSYVVVELLRSFFVTETTFQKNRLFYRKSVMSKLSQIGIROHLKRVOLRE 600

Qy 601 LSEAEVROHREARPALTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPALTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy 661 LFSVLNTERARRPGLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PODRLTEVIASIIKPQNTYCYRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFOVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCYRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFOVAHL 780

Qy 781 QETSPLDADVIEQSSLINEASSGLFDVFLRFMCHAVIRIGKSVYVOCQGIPOGSIISLT 840
Db 781 QETSPLDADVIEQSSLINEASSGLFDVFLRFMCHAVIRIGKSVYVOCQGIPOGSIISLT 840

Qy 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVLTPLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVLTPLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy 901 RKTVYNPFVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVDQSDYSYARTSIRASLT 960
Db 901 RKTVYNPFVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVDQSDYSYARTSIRASLT 960
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Qy 961 NRGFKAGRNRRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
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Qy 1021 FHOQVKNPTFFELRVISDTASLCYSILKAKNAGNSLGAAGAAGPLPSEAVQWLCHQAFLL 1080
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Qy 1081 KLTRHRYVYVPLLGSLRTAQTLQSRKLP GTTTLTALEAAANPALPSDFKTTILD 1132
Db 1081 KLTRHRYVYVPLLGSLRTAQTLQSRKLP GTTTLTALEAAANPALPSDFKTTILD 1132

RESULT 5
US-09-128-354-2
; Sequence 2, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310US
; CURRENT APPLICATION NUMBER: US/09/128,354
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-354-2

Query Match      100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQRGDDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPCRAVRSLLRSHYREVLPLATFVRRLLGPGQWRLVQRGDDPAAFRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSPROVSCSKELVARVLQRLCERGAKNVLAFGFPALLDGGARGGPEAFTTSVR 120
Db 61 DARPPPAAPSPROVSCSKELVARVLQRLCERGAKNVLAFGFPALLDGGARGGPEAFTTSVR 120

Qy 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180

Qy 181 ATQARPPHAGSPRRRLGCCRANVHNSVREAGVPLGLPAPGARRRGGSGASRSLPLPKPRR 240
Db 181 ATQARPPHAGSPRRRLGCCRANVHNSVREAGVPLGLPAPGARRRGGSGASRSLPLPKPRR 240

Qy 241 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVSPARPABEATSLEGALSGTRHSHPSVG 300
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Db 241 GAAPEPRTVQGSWAHPGRTRGSDRGFCVVSPPARPAEBATSLEGALSGTRHSHPSVG 300
QY 301 ROHHAGPSTSPRPDPWDTCPVVAETKHFLYSSGDEQELRPSFLLSSLPSTTGARRL 360
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QY 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERFRUNTKKFTISLGKHAKLISQELTWKMSVRDCAWLRRSPGVCPVAAEHLREEI 540
Db 481 RHNERFRUNTKKFTISLGKHAKLISQELTWKMSVRDCAWLRRSPGVCPVAAEHLREEI 540
QY 541 LAKFLHLMWSVVVVELLRASFFVYVTTTFFQKNRLFYRKSVMSKLQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHLMWSVVVVELLRASFFVYVTTTFFQKNRLFYRKSVMSKLQSIGIRQHLKRVOLRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNVERAARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERAARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDADVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
Db 781 QETSPLRDADVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
QY 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGPYEGCVNVL 900
Db 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGPYEGCVNVL 900
QY 901 RKTWNVPVDEALGGTAFVQMPAHGLFPWCGLLDTRTILEVQSDYSSVARTSIRASLTF 960
Db 901 RKTWNVPVDEALGGTAFVQMPAHGLFPWCGLLDTRTILEVQSDYSSVARTSIRASLTF 960
QY 961 NRGFKAGRNRRKLPFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1020
Db 961 NRGFKAGRNRRKLPFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1020
QY 1021 FHOQVKNPFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFL 1080
Db 1021 FHOQVKNPFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFL 1080
QY 1081 KLTHRRVYVPLLGSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTHRRVYVPLLGSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTILD 1132

RESULT 6
US-09-675-321-2
; Sequence 2, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006

; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-675-321-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60
QY 61 DARPPPAAPSPQVSCICKELVARVQLRCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
Db 61 DARPPPAAPSPQVSCICKELVARVQLRCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
QY 121 SYLPTNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYOVCGPPLYOLGA 180
Db 121 SYLPTNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYOVCGPPLYOLGA 180
QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGAPGARRRRGGSASRSLLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGAPGARRRRGGSASRSLLPKRPRR 240
QY 241 GAAPEPRTVQGSWAHPGRTRGSDRGFCVVSPPARPAEBATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPRTVQGSWAHPGRTRGSDRGFCVVSPPARPAEBATSLEGALSGTRHSHPSVG 300
QY 301 ROHHAGPSTSPRPDPWDTCPVVAETKHFLYSSGDEQELRPSFLLSSLPSTTGARRL 360
Db 301 ROHHAGPSTSPRPDPWDTCPVVAETKHFLYSSGDEQELRPSFLLSSLPSTTGARRL 360
QY 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERFRUNTKKFTISLGKHAKLISQELTWKMSVRDCAWLRRSPGVCPVAAEHLREEI 540
Db 481 RHNERFRUNTKKFTISLGKHAKLISQELTWKMSVRDCAWLRRSPGVCPVAAEHLREEI 540
QY 541 LAKFLHLMWSVVVVELLRASFFVYVTTTFFQKNRLFYRKSVMSKLQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHLMWSVVVVELLRASFFVYVTTTFFQKNRLFYRKSVMSKLQSIGIRQHLKRVOLRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNVERAARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERAARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDADVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
Db 781 QETSPLRDADVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
QY 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGPYEGCVNVL 900
Db 841 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGPYEGCVNVL 900

Db 841 LCSICYGDMENKLFAGIRRDGILLRLVDDFLLVTHLTHAKTFLRTLVRGVPEYGCVVNL 900
Qy 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASITF 960
Db 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASITF 960
Qy 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLDQNSLQTVCTNTYKILLQAYRFHACVQLQP 1020
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLDQNSLQTVCTNTYKILLQAYRFHACVQLQP 1020
Qy 1021 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGSLRTAQTQLSRKLPGLTTLTALAANAALPSPDFKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQTQLSRKLPGLTTLTALAANAALPSPDFKTILD 1132

RESULT 7
US-09-052-919-2
; Sequence 2, Application US/09052919
; Patent No. 644650
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,919
; FILING DATE: 31-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17895
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-003600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-052-919-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLPGOCWELVORGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLPGOCWELVORGDPAAFRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSRQVSCIKELVARVLQRLCERGANVLAFFALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSRQVSCIKELVARVLQRLCERGANVLAFFALLDARGGPEAFTTSVR 120

Qy 121 SYLPTNTVDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYLQGA 180
Db 121 SYLPTNTVDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYLQGA 180

Qy 181 ATQARPPPHASGPRRLRGCRANVHVSREAGVPLGLPAGARRRGSSASRSLPLPKPRR 240
Db 181 ATQARPPPHASGPRRLRGCRANVHVSREAGVPLGLPAGARRRGSSASRSLPLPKPRR 240

Qy 241 GAAPEPERTPVGGGSAHPGRTGRGSDRGFCVSPARPABEATSEALSGTRHSHPSVG 300
Db 241 GAAPEPERTPVGGGSAHPGRTGRGSDRGFCVSPARPABEATSEALSGTRHSHPSVG 300

Qy 301 RQHAGPSTSRPRPMDTFCPPVYAEKHLVSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTFCPPVYAEKHLVSSGDKQLRPSFLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRPMPGTPRRLPRLPORYWQMRPLFLELGNHAQCYPYVLLKTHCPLEAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPORYWQMRPLFLELGNHAQCYPYVLLKTHCPLEAAVT 420

Qy 421 PAAGVCAREKPOGSAVAPEEEDTDPRRLVQLLRQHSPPQWYGVFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSAVAPEEEDTDPRRLVQLLRQHSPPQWYGVFVRACLRLVPPGLWGS 480

Qy 481 RHNERFLRNTKKFIISLGKIAKLSLOELTWKMSVDCAWLRRSPGVCGVPAAEHRLREEI 540
Db 481 RHNERFLRNTKKFIISLGKIAKLSLOELTWKMSVDCAWLRRSPGVCGVPAAEHRLREEI 540

Qy 541 LAKFHLWLMVYVVELLRSFFYVTTTFOKNLFFYFKSVKSLQSIGIRHKLKRVOLRE 600
Db 541 LAKFHLWLMVYVVELLRSFFYVTTTFOKNLFFYFKSVKSLQSIGIRHKLKRVOLRE 600

Qy 601 LSEAEVQRHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRYKA 660

Db 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNDVYVGARTFRREKGAERLTSRVA 660
QY 661 LFSVLNVERARPGILGASVLGDDHRAWRTFVLRAQDPPBELYFKVDVDTGAYDTI 720
Db 661 LFSVLNVERARPGILGASVLGDDHRAWRTFVLRAQDPPBELYFKVDVDTGAYDTI 720
QY 721 PDRLTEVIASIIKQNTYCVARYAVVQAAHGHVRKAFKSHVSTLTDLPVMOQFVAHL 780
Db 721 PDRLTEVIASIIKQNTYCVARYAVVQAAHGHVRKAFKSHVSTLTDLPVMOQFVAHL 780
QY 781 QETSPURDAVITEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVVQCQIGPOQSILSTL 840
Db 781 QETSPURDAVITEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVVQCQIGPOQSILSTL 840
QY 841 LCSLCYGDMEKLFAGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPYEGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPYEGCVVNL 900
QY 901 RKTVVNFVDEBALGCTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSYARTSIRASLTF 960
Db 901 RKTVVNFVDEBALGCTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSYARTSIRASLTF 960
QY 961 NRGFAGNMRKLFVLRKCHSLFLDLQNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
Db 961 NRGFAGNMRKLFVLRKCHSLFLDLQNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
QY 1021 FHQQWKNPTFFLRVISDASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPGLTTLTAAEAAANPALPSPDKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPGLTTLTAAEAAANPALPSPDKTILD 1132

RESULT 8

US-08-912-951-2
; Sequence 2, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLLVQRGDPAAFRALVAQCLVCPWM 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLLVQRGDPAAFRALVAQCLVCPWM 60
QY 61 DARPPAAPSPFQVSCLELVARVLRQRCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
Db 61 DARPPAAPSPFQVSCLELVARVLRQRCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGANGLLLRVDDVLVHLLARCALFVLVAPSCAVQVCGPPLYLGA 180
Db 121 SYLPTNTVDALRGSGANGLLLRVDDVLVHLLARCALFVLVAPSCAVQVCGPPLYLGA 180
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QY 301 RQHAGPSTSRPPRWDTPCPVYAEAKHFLYSSGDKQOLRPSFLLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRWDTPCPVYAEAKHFLYSSGDKQOLRPSFLLSSLRPSLTGARRL 360
QY 361 VETIFLSRPMPTGTPRRLLPRLPORYQMRPLFLELLGNHACQPYGVLLKTHCPRAAVT 420
Db 361 VETIFLSRPMPTGTPRRLLPRLPORYQMRPLFLELLGNHACQPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQHSPPWOVGFVACILRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQHSPPWOVGFVACILRLVPPGLWGS 480
QY 481 RHNERFRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAASHRLREEI 540
Db 481 RHNERFRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAASHRLREEI 540
QY 541 LAKFLHMLMSVYVVELLSRFFYTETTFQKNRFFYRKSVWSKLQIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLMSVYVVELLSRFFYTETTFQKNRFFYRKSVWSKLQIGIRQHLKRVOLRE 600

Qy 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRYKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAODPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAODPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTLQPYMQFVAHL 780
Db 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTLQPYMQFVAHL 780
Qy 781 QETSPLRDAVIEOSSSINEASSGLFVFLRPMCHHAVIRGKSVVQCQIPQSGIISLTL 840
Db 781 QETSPLRDAVIEOSSSINEASSGLFVFLRPMCHHAVIRGKSVVQCQIPQSGIISLTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTEFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTEFLRTLVRGVPEYGCVVNL 900
Qy 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSYARTSIRASITF 960
Db 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSYARTSIRASITF 960
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFIDLQNSLQTVCTNIIKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFIDLQNSLQTVCTNIIKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQWKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQWKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPQTTLTALAAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPQTTLTALAAAANPALPSDFKTILD 1132

RESULT 9

US-09-402-181B-2
; Sequence 2, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausehuse, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-402-181B-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWELVORGDDPAARFALVAQCLVCPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWELVORGDDPAARFALVAQCLVCPW 60

Qy 61 DARPPPAAPSFROVSCCLKELVARVLQRCERGAKNVLAFAFALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSFROVSCCLKELVARVLQRCERGAKNVLAFAFALLDARGGPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGRRRLGRCERANNHVSREAGVPLGLPAPGARREGGASRSLLPKPRR 240
Db 181 ATQARPPPHASGRRRLGRCERANNHVSREAGVPLGLPAPGARREGGASRSLLPKPRR 240

Qy 241 GAAPEPERTPVQGSWAHPGRTGRPSDRGFCVWSPARPABEATSEALSGTRHSHPSVG 300
Db 241 GAAPEPERTPVQGSWAHPGRTGRPSDRGFCVWSPARPABEATSEALSGTRHSHPSVG 300

Qy 301 RQHAGPPSTSRPPRMDTPCPVYAEKHFVYSSGDKQLRPSFLLSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPRMDTPCPVYAEKHFVYSSGDKQLRPSFLLSLRPSLTGARRL 360

Qy 361 VETIFLGSRWMPGCTPRRLPRLPQRYWQMPLELLELGNHAOCYPGVLLKTHCPRLRAVT 420
Db 361 VETIFLGSRWMPGCTPRRLPRLPQRYWQMPLELLELGNHAOCYPGVLLKTHCPRLRAVT 420

Qy 421 PAAGVCAREKXPGQSVAAPEEEDTPRLVLQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKXPGQSVAAPEEEDTPRLVLQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480

Qy 481 RHNERRFLRNTKXFIISLGKHAQLSLQELTWKMSVRCDAWLRRSPGVGCVPAAEHLREEI 540
Db 481 RHNERRFLRNTKXFIISLGKHAQLSLQELTWKMSVRCDAWLRRSPGVGCVPAAEHLREEI 540

Qy 541 LAKFLHMLMSVYVVELLRSPFYTTETFOKNRLFYFRKSVWSKLQSIGIRQHLKRVQJRE 600
Db 541 LAKFLHMLMSVYVVELLRSPFYTTETFOKNRLFYFRKSVWSKLQSIGIRQHLKRVQJRE 600

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Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDVVGARTFREKRAERLTSRVKA 660
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Db 661 LFSVLNVERARRPGLGASVLGLDDIHRAMRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
QY 721 PQDRLTEVIASIIKPNQTYCVRRAVAVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PQDRLTEVIASIIKPNQTYCVRRAVAVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
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Db 841 LCSLCYGMENKIFAGIRRDGLLRLVDDFLVTPHILTHAKTFILRTILVRGVPEYGCVVNL 900
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QY 961 NRGFKAGNNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
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QY 1021 PHQOVKNPTFFLRFVSDTASLCYSIILKAKNAGSLGAKAAGPLPSEAVQWLCHQAFLL 1080
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QY 1081 KLTRHRTVYVPLGLSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTLTD 1132
Db 1081 KLTRHRTVYVPLGLSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTLTD 1132

RESULT 10

US-09-721-456-2
; Sequence 2, Application US/09721456
; Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-NOV-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-721-456-2

Query Match

Best Local Similarity 100.0%; Score 5961; DB 4; Length 1132;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVORGDPAAFRALVAQCLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVORGDPAAFRALVAQCLVCVPM 60
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Db 61 DARPPPAAPSFQVSKLKVRLQRCERGAQKVLAFGPFALLDGAAGPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRGGSASRSLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRGGSASRSLPKRPRR 240
QY 241 GAAPEPERTPVQGGSWAHPGTRGSDRGFCVVSAPAEAEATSLEGALSGRTRHSHPSVG 300
Db 241 GAAPEPERTPVQGGSWAHPGTRGSDRGFCVVSAPAEAEATSLEGALSGRTRHSHPSVG 300
QY 301 RQHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
QY 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSEPMQVYGFVRACLRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSEPMQVYGFVRACLRLVPPGLMGS 480
QY 481 RHNERFLRNTKKFISLGNHAKLSLOELTWKSVRDCAWLRSPGCVGCPAAEHLRBEI 540
Db 481 RHNERFLRNTKKFISLGNHAKLSLOELTWKSVRDCAWLRSPGCVGCPAAEHLRBEI 540

Qy 541 LAKFLHLMMSVYVVELLBSFFYVTTTQKRLRPFYKSVMSKQSIGIROHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLBSFFYVTTTQKRLRPFYKSVMSKQSIGIROHLKRVQRE 600
Qy 601 LSEAEVRHREARPALTSRLRFPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRHREARPALTSRLRFPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLRVRAQPPPELYFKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLRVRAQPPPELYFKVDVTGAYDTI 720
Qy 721 PQDLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 721 PQDLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Qy 781 QETSPLRDAVIEOSSLINEASSGLFDVFLPMCHAVRIRGKSVQCQGIPOGSIILSTL 840
Db 781 QETSPLRDAVIEOSSLINEASSGLFDVFLPMCHAVRIRGKSVQCQGIPOGSIILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTVVNPFVEALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQDSYARTSRASLTF 960
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Qy 961 NRGFKAGNMRKLPVLRKCHSLFDLQVNSLQTVCTNLYKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLPVLRKCHSLFDLQVNSLQTVCTNLYKILLQAYRPHACVLQLP 1020
Qy 1021 FHQQVKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Db 1021 FHQQVKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Qy 1081 KLTHRVTVYPLGLSLRTAQQLSRKLPDGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVYPLGLSLRTAQQLSRKLPDGTTLTALAAANPALPSDFKTILD 1132

RESULT 11
US-09-953-052-2
; Sequence 2, Application US/09953052
; Patent No. 6627619
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,052
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/052,919
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-0036000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPLATFVRRLPGQWRLVQKGDPAAPRALVAQCLVCVPW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPLATFVRRLPGQWRLVQKGDPAAPRALVAQCLVCVPW 60
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Db 121 SYLNTVTDALRGSGAWGLLRLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
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Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAGARRRGGASRSLPLPKPRR 240
Qy 241 GAAPEPERTPVQGSWAHPGRTGRPSDRGFCVSWPARPABEATSLGALSGTRHSHPSVG 300
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Db 481 RHNERFLRNTKKFISLGKHAKLQSLBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
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Qy 601 LSEAEVQRHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSVKKA 660
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Qy 841 LCSLCYGDMMENKLFAGIRROGLLRLVDDFLVTPHLLTHAKTHLRTLVRGVPEYGCVVNL 900
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Db 1081 KLTRHRVTVYVPLGLSLRTAQTQLSRKLPGTTLTALEAANPALPSPDKTILD 1132

RESULT 12
US-09-042-460-3
; Sequence 3, Application US/09042460
; Patent No. 6767719
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Allsopp, Richard
; APPLICANT: Depinho, Ronald
; APPLICANT: Greenberg, Roger
; TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,460

; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA: US 08/979,742
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 015389-003110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1132
; OTHER INFORMATION: /note="human telomerase reverse
; OTHER INFORMATION: transcriptase (hTRT)"
US-09-042-460-3

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPRAFPCRAVRSLLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAOCLVCVPW 60

Qy 61 DARPPPAAPSPFQVSCCLKELVARLQRLCERGAKNVLAFGFALLDGCARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSPFQVSCCLKELVARLQRLCERGAKNVLAFGFALLDGCARGGPPPEAFTTSVR 120

LOCATION: 1..1154
OTHER INFORMATION: /notes="fusion protein composed of hTERT
OTHER INFORMATION: protein sequence, vector sequences, the
OTHER INFORMATION: Myc epitope and His6 tag"
US-08-974-549A-611

Query Match 100.0%; Score 5961; DB 3; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHYREVLPATFVRRIGPQGRVLRVQDGPAAFPALVAQCLVCPV 60
Db 1 MPAPRCRAVSLRSHYREVLPATFVRRIGPQGRVLRVQDGPAAFPALVAQCLVCPV 60

QY 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120
Db 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASRRRLGCEAWNHSVREAGVPLGLPAGARRRGGASRLPLPKPRR 240
Db 181 ATQARPPPHASRRRLGCEAWNHSVREAGVPLGLPAGARRRGGASRLPLPKPRR 240

QY 241 GAAPERTPVQGSWAHPGRTGRPSDRGFCVSPAPAEATSLGALSCTRHSHPVSG 300
Db 241 GAAPERTPVQGSWAHPGRTGRPSDRGFCVSPAPAEATSLGALSCTRHSHPVSG 300

QY 301 ROHAGPPSTSRPPMDTPCPVYAEKHFYSSGDKQLRPSFLSLRPSLTGARRL 360
Db 301 ROHAGPPSTSRPPMDTPCPVYAEKHFYSSGDKQLRPSFLSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMCTPRRLPRLPORYWQMRPLFELIGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRRPMCTPRRLPRLPORYWQMRPLFELIGNHAQCPYGVLLKTHCPRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRHSSPMQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRHSSPMQVYGFVRACLRLVPPGLWGS 480

QY 481 RHNERRLRNTKFIISLGKAKLSQLBLTWKMSVRDCAWLRSPGVCVPAABHRLREEI 540
Db 481 RHNERRLRNTKFIISLGKAKLSQLBLTWKMSVRDCAWLRSPGVCVPAABHRLREEI 540

QY 541 LAKEFLHLMSSVYVELLRSFFYVTEITFQKNRFFYKSVWSKLSQIGIRQHLLKRVOLRE 600
Db 541 LAKEFLHLMSSVYVELLRSFFYVTEITFQKNRFFYKSVWSKLSQIGIRQHLLKRVOLRE 600

QY 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660

QY 661 LFSVLNVERARRCLLGASVLGLDDTHRAWRTFVLVRAQDPPPELYFKVDVGTGAYDTI 720
Db 661 LFSVLNVERARRCLLGASVLGLDDTHRAWRTFVLVRAQDPPPELYFKVDVGTGAYDTI 720

QY 721 PQDLTEVIAIISKPNQTYCVRYAVVQKAHGHVKAFAKSHVSTLTDLQPMYRQFVAHL 780
Db 721 PQDLTEVIAIISKPNQTYCVRYAVVQKAHGHVKAFAKSHVSTLTDLQPMYRQFVAHL 780

QY 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYQCGI PQGSILSTL 840
Db 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYQCGI PQGSILSTL 840

QY 841 LCSLCYGDMEKLFAGIRDGLLLRLVDDPLVTPHITAKTFLRLVRGVEYGCNNL 900
Db 841 LCSLCYGDMEKLFAGIRDGLLLRLVDDPLVTPHITAKTFLRLVRGVEYGCNNL 900

QY 901 RKTWNVPFVEDEALGGTAFQMPAHGLFPWCGLLDDTRTLEVQSDYSSVARTSIRASLTF 960
Db 901 RKTWNVPFVEDEALGGTAFQMPAHGLFPWCGLLDDTRTLEVQSDYSSVARTSIRASLTF 960

QY 961 NRGFKAGNNRRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db 961 NRGFKAGNNRRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020

QY 1021 FHOQVKNPTFFELRVISDTSASLCYSTILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHOQVKNPTFFELRVISDTSASLCYSTILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTHRVTVYVPLGLSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTLID 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTLID 1132

RESULT 14
US-08-912-951-323
; Sequence 323, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 323:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-323

Query Match      100.0%; Score 5961; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 DARPPAAPSPROVSKELVARVLQRLCERAGKNVLAFFGALLDARGGPEAFTTSVR 120
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Qy 121 SYLPTVTDALRGSGAGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTVTDALRGSGAGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATOARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKPRR 240
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Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300
Db 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300

Qy 301 RQHAGPSTSRPRPMDTPCPPVYAEKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPPVYAEKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRPMPGTTPRLPLPORYQMRLPFLLELGNHAQCYPYVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTTPRLPLPORYQMRLPFLLELGNHAQCYPYVLLKTHCPRAAVT 420

Qy 421 PAAGVCAREKPGSVAAPPEEDTPRLVQLLRHSSPWQYVGVFRACLRRLVPPGLWS 480
Db 421 PAAGVCAREKPGSVAAPPEEDTPRLVQLLRHSSPWQYVGVFRACLRRLVPPGLWS 480

Qy 481 RHNERRFLRNTKFIISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCPVAAEHLREEI 540
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Qy 541 LAKFLHLMMSYVVVELLRSFPYVTTFTFQKNRLLPFYRKSVMSKLQSIGIRQHLKRVQRE 600
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Qy 601 LSEAEVQHRERARPAALTSRLRFTPKDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660
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Qy 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780

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Db 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVOCQGIPOQSILSTL 840

Qy 841 LCSLCYGDMEKNKLFAGIRRDGLLRVDDPLLVTPHLTHAKTFLTRVGRVPEYGCVVNL 900
Db 841 LCSLCYGDMEKNKLFAGIRRDGLLRVDDPLLVTPHLTHAKTFLTRVGRVPEYGCVVNL 900

Qy 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDYSSYARTSIRASLTF 960
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RESULT 15

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US-09-402-181B-611
; Sequence 611, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin B.
;             Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402.181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /notes="fusion protein composed of hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-09-402-181B-611

Query Match 100.0%; Score 5961; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MPAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRLVQRGDDPAAPRALVAQCLVCVPW 60

QY 61 DARPPPAAPSROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
DB 61 DARPPPAAPSROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAVQVCGPELYOLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAVQVCGPELYOLGA 180

QY 181 ATQARPPPHASGPRRRRLCERAMNHSVREAGVPLGLPAGARRRGSGASRLPLPKPRR 240
DB 181 ATQARPPPHASGPRRRRLCERAMNHSVREAGVPLGLPAGARRRGSGASRLPLPKPRR 240

QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVWSPARPAEATSEALSGTRHSHPSVG 300
DB 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVWSPARPAEATSEALSGTRHSHPSVG 300

QY 301 RQHAGPSTSRPPRPMWDTCPFPVYAEYKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
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QY 361 VETIFLGSRRPMPTGPRRLPRLPORVQWMPLELLGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPTGPRRLPRLPORVQWMPLELLGNHAQCPYGVLLKTHCPLRAAVT 420

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DB 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLRQHSPPQVYGFVRACLRLVPPGLWGS 480

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QY 541 LAKFLHLMWSYVVELLSRFYVTTETFOKNRLFYRKSVWSKLQSIGIRQHLKRVQURE 600
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QY 601 LSEAEVRQHREARPAALLTSRLRPIPKPDGLRPIVNMNDYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRPIPKPDGLRPIVNMNDYVVGARTFRREKRAERLTSRVKA 660

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DB 661 LFSVLNVERARRPGLLGASVLGDDIHRAWRTFVLRAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PDRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVKAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PDRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVKAFKSHVSTLTDLOPYMRQFVAHL 780

QY 781 QETSPLRDVAVIEQSSLINEASGLFDVFLRFMCHHAVRIRGKSVYVQCQGIPOGSIILSTL 840
DB 781 QETSPLRDVAVIEQSSLINEASGLFDVFLRFMCHHAVRIRGKSVYVQCQGIPOGSIILSTL 840
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DB 781 QETSPLRDVAVIEQSSLINEASGLFDVFLRFMCHHAVRIRGKSVYVQCQGIPOGSIILSTL 840
QY 841 LCSLCYGD MENKLFAGIRRDG LLLRLVDDFLVTPH LTHAKTFLRTLVRGVPYGCVVNL 900
DB 841 LCSLCYGD MENKLFAGIRRDG LLLRLVDDFLVTPH LTHAKTFLRTLVRGVPYGCVVNL 900
QY 901 RKTVVNFPVDEDEALGGTAFVQMPAHGLFPWCGLLLDLTRLLEVQSDYSSYARTSIRASLTF 960
DB 901 RKTVVNFPVDEDEALGGTAFVQMPAHGLFPWCGLLLDLTRLLEVQSDYSSYARTSIRASLTF 960
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DB 961 NRGFKAGRNMRRLFGVLR LKCHSLFLDLQVNSLQVCTNIYKILLQAYRFHACVQLP 1020
QY 1021 FHQQVWKNFTFFLRVISDTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHOAFLL 1080
DB 1021 FHQQVWKNFTFFLRVISDTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWLCHOAFLL 1080
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DB 1081 KLTRHRVTYVPLLGSLRTAQ TOLSRKLPQTTLTAL EAAANPALPSDFKTILD 1132
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